

Result No.	Score	Query Match	Length	DB ID	Description
1	3321	100.0	619	4	US-10-763-179-12
2	3321	100.0	619	5	US-10-849-814-12
3	3321	100.0	619	5	US-10-855-533-12
4	3321	100.0	619	5	US-10-859-405-12
5	3321	100.0	619	5	US-10-876-673-12
6	3321	100.0	619	6	US-11-050-829-20
7	2198.5	66.2	616	4	US-10-763-179-6
8	2198.5	66.2	616	5	US-10-849-814-6
9	2198.5	66.2	616	5	US-10-855-533-6
10	2198.5	66.2	616	5	US-10-859-405-6
11	2198.5	66.2	616	5	US-10-876-673-6
12	2198.5	66.2	616	6	US-11-050-829-14
13	2198.5	66.2	616	6	US-11-085-576-12
14	2187.5	65.9	594	6	US-11-085-576-3
15	2081	62.7	625	4	US-10-763-179-18
16	2081	62.7	625	5	US-10-855-533-18
17	2081	62.7	625	5	US-10-876-673-18
18	1618	48.7	645	4	US-10-763-179-23
19	1618	48.7	645	5	US-10-855-533-23
20	1618	48.7	645	5	US-10-876-673-23
21	1402.5	42.2	644	4	US-10-763-179-27
22	1402.5	42.2	644	5	US-10-855-533-27
23	1402.5	42.2	644	5	US-10-876-673-27
24	1402	42.2	620	4	US-10-763-179-25
25	1402	42.2	620	5	US-10-855-533-25
26	1402	42.2	620	5	US-10-876-673-25
27	356	10.7	549	5	US-10-482-706-197

Qy 301 AYGTFKTYQSIEDKSCKNNNSILVAGPWWHGGWVRAGNYLCDIQPEKKTSITYQEQFQP 360
 Db 301 AYGTFKTYQSIEDKSCKNNNSILVAGPWWHGGWVRAGNYLCDIQPEKKTSITYQEQFQP 360
 Qy 361 FPKYYLKDDEGNFAPSEANIFVGSNEWKHFEEQWPKNVETKLYFOPQGKLGFDFKVQRTD 420
 Db 361 FPKYYLKDDEGNFAPSEANIFVGSNEWKHFEEQWPKNVETKLYFOPQGKLGFDFKVQRTD 420
 Qy 421 SWDEYTTDPNKEPVPHOGVIONTRTEYMDVDDORFAASRPDVMYQTEPLTIVGPICK 480
 Db 421 SWDEYTTDPNKEPVPHOGVIONTRTEYMDVDDORFAASRPDVMYQTEPLTIVGPICK 480
 Qy 481 NFLKVSSSTGTDADYVVKLIDVYVNLDAASYCQKTMACYQMVTRGEIMAGKYRNGFDKAQAL 540
 Db 481 NFLKVSSSTGTDADYVVKLIDVYVNLDAASYCQKTMACYQMVTRGEIMAGKYRNGFDKAQAL 540
 Qy 541 TPGMVEKVNFMEMPDAHTFKKGHRIMVQVONSWFLAERNPQFLAPYATKADFRKATQ 600
 Db 541 TPGMVEKVNFMEMPDAHTFKKGHRIMVQVONSWFLAERNPQFLAPYATKADFRKATQ 600
 Qy 601 RIFHDVNNATYIEFSVLD 619
 Db 601 RIFHDVNNATYIEFSVLD 619

RESULT 2
 US-10-849-814-12
 ; Sequence 12, Application US/10849814
 ; PUBLICATION NO. US20040219631A1
 ; GENERAL INFORMATION:
 ; APPLICANT: YOKOZEKI, KENZO
 ; APPLICANT: SUZUKI, SONOKO
 ; APPLICANT: HARA, SEIICHI
 ; APPLICANT: ABE, ISAO
 ; TITLE OF INVENTION: METHOD FOR PRODUCING TRIPETIDES AND/OR PEPTIDES LONGER THAN TRIPETIDE REFERENCE: 25230BUS0CONT
 ; CURRENT APPLICATION NUMBER: US/10/849,814
 ; CURRENT FILING DATE: 2004-05-21
 ; PRIOR APPLICATION NUMBER: PCT/JP03/09466
 ; PRIOR FILING DATE: 2003-07-25
 ; PRIOR APPLICATION NUMBER: JP 2002-218958
 ; PRIOR FILING DATE: 2002-07-26
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 12
 ; LENGTH: 619
 ; TYPE: PRT
 ; ORGANISM: Sphingobacterium sp.
 US-10-849-814-12

Query Match Score 3321; DB 5; Length 619;
 Best Local Similarity 100.%; Pred. No. 3.2e-260;
 Matches 619; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 MKNTISCLTLLASQHQTAADSAYVRDHYEKEVAFMRDGKLLFPAIYSPKDLSK 60
 Db 1 MKNTISCLTLLASQHQTAADSAYVRDHYEKEVAFMRDGKLLFPAIYSPKDLSK 60
 Qy 61 KYPVLLNRTPYTSPYGCQNEYTKSLGNFPQMREGYIFTYDVRGKMSGDFEDIRPTT 120
 Db 61 KYPVLLNRTPYTSPYGCQNEYTKSLGNFPQMREGYIFTYDVRGKMSGDFEDIRPTT 120
 Qy 121 YSKDKKAIDESTDTYDALEWLOKLNLYKNGKAGIYGLSYPGFYSTVGLWTHPSLKAVSP 180
 Db 121 YSKDKKAIDESTDTYDALEWLOKLNLYKNGKAGIYGLSYPGFYSTVGLWTHPSLKAVSP 180
 Qy 181 QAPTDWYIGDDFHANGVLFLQDAFTFMSITPGVPRKPIPDQFGKQIKQKEADKYNPFA 240
 Db 181 QAPTDWYIGDDFHANGVLFLQDAFTFMSITPGVPRKPIPDQFGKQIKQKEADKYNPFA 240
 Qy 241 EAGTARELKEYFQDSVQFWNDLFKHFDYDDFWKSRVITNSLOEVPAVMVGGFFDAED 300
 Db 241 EAGTARELKEYFQDSVQFWNDLFKHFDYDDFWKSRVITNSLOEVPAVMVGGFFDAED 300

Qy 301 AYGTFKTYQSIEDKSCKNNNSILVAGPWWHGGWVRAGNYLCDIQPEKKTSITYQEQFQP 360
 Db 301 AYGTFKTYQSIEDKSCKNNNSILVAGPWWHGGWVRAGNYLCDIQPEKKTSITYQEQFQP 360
 Qy 361 FPKYYLKDDEGNFAPSEANIFVGSNEWKHFEEQWPKNVETKLYFOPQGKLGFDFKVQRTD 420
 Db 361 FPKYYLKDDEGNFAPSEANIFVGSNEWKHFEEQWPKNVETKLYFOPQGKLGFDFKVQRTD 420
 Qy 421 SWDEYTTDPNKEPVPHOGVIONTRTEYMDVDDORFAASRPDVMYQTEPLTIVGPICK 480
 Db 421 SWDEYTTDPNKEPVPHOGVIONTRTEYMDVDDORFAASRPDVMYQTEPLTIVGPICK 480
 Qy 481 NFLKVSSSTGTDADYVVKLIDVYVNLDAASYCQKTMACYQMVTRGEIMAGKYRNGFDKAQAL 540
 Db 481 NFLKVSSSTGTDADYVVKLIDVYVNLDAASYCQKTMACYQMVTRGEIMAGKYRNGFDKAQAL 540
 Qy 541 TPGMVEKVNFMEMPDAHTFKKGHRIMVQVONSWFLAERNPQFLAPYATKADFRKATQ 600
 Db 541 TPGMVEKVNFMEMPDAHTFKKGHRIMVQVONSWFLAERNPQFLAPYATKADFRKATQ 600
 Qy 601 RIFHDVNNATYIEFSVLD 619
 Db 601 RIFHDVNNATYIEFSVLD 619

RESULT 3
 US-10-855-533-12
 ; Sequence 12, Application US/10855533
 ; Publication No. US20050019864A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HARA, SEIICHI
 ; APPLICANT: YOKOZEKI, KENZO
 ; APPLICANT: ABE, ISAO
 ; APPLICANT: TONOUCHI, NAOTO
 ; APPLICANT: JOJIMA, YASURO
 ; TITLE OF INVENTION: NOVEL PEPTIDE-FORMING ENZYME GENES
 ; CURRENT APPLICATION NUMBER: US/10/855,533
 ; CURRENT FILING DATE: 2004-05-28
 ; PRIOR APPLICATION NUMBER: PCT/JP03/09468
 ; PRIOR FILING DATE: 2003-07-25
 ; PRIOR APPLICATION NUMBER: JP 2002-218957
 ; PRIOR FILING DATE: 2002-07-26
 ; PRIOR APPLICATION NUMBER: JP 2003-16765
 ; PRIOR FILING DATE: 2003-07-24
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 12
 ; LENGTH: 619
 ; TYPE: PRT
 ; ORGANISM: Sphingobacterium sp.
 US-10-855-533-12

Query Match Score 3321; DB 5; Length 619;
 Best Local Similarity 100.%; Pred. No. 3.2e-260;
 Matches 619; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 MKNTISCLTLLASQHQTAADSAYVRDHYEKEVAFMRDGKLLFPAIYSPKDLSK 60
 Db 1 MKNTISCLTLLASQHQTAADSAYVRDHYEKEVAFMRDGKLLFPAIYSPKDLSK 60
 Qy 61 KYPVLLNRTPYTSPYGCQNEYTKSLGNFPQMREGYIFTYDVRGKMSGDFEDIRPTT 120
 Db 61 KYPVLLNRTPYTSPYGCQNEYTKSLGNFPQMREGYIFTYDVRGKMSGDFEDIRPTT 120
 Qy 121 YSKDKKAIDESTDTYDALEWLOKLNLYKNGKAGIYGLSYPGFYSTVGLWTHPSLKAVSP 180
 Db 121 YSKDKKAIDESTDTYDALEWLOKLNLYKNGKAGIYGLSYPGFYSTVGLWTHPSLKAVSP 180
 Qy 181 QAPTDWYIGDDFHANGVLFLQDAFTFMSITPGVPRKPIPDQFGKQIKQKEADKYNPFA 240
 Db 181 QAPTDWYIGDDFHANGVLFLQDAFTFMSITPGVPRKPIPDQFGKQIKQKEADKYNPFA 240
 Qy 241 QAPTDWYIGDDFHANGVLFLQDAFTFMSITPGVPRKPTPDPQFGKQIKQKEADKYNFFA 240
 Db 241 QAPTDWYIGDDFHANGVLFLQDAFTFMSITPGVPRKPTPDPQFGKQIKQKEADKYNFFA 240

Qy 241 EAGTARELKEKYFGDSVQFWNDLFKHPDYDDENFKSRVITNSLQEVKPAVMVGGFPDAED 300
Db 241 EAGTARELKEKYFGDSVQFWNDLFKHPDYDDENFKSRVITNSLQEVKPAVMVGGFPDAED 300
Qy 301 AYGTFTKTVQSIEDKSCKNSILVAGPWHGGWTRAEGNYLGDQFEKTSITYQBQFQP 360
Db 301 AYGTFTKTVQSIEDKSCKNSILVAGPWHGGWTRAEGNYLGDQFEKTSITYQBQFQP 360
Qy 361 FPKXYLKDEGNFAPSEANIFVSSSNNEWHFBOMPCKNTEVETKLYFQPGKLGFDKVQRTD 420
Db 361 FPKXYLKDEGNFAPSEANIFVSSSNNEWHFBOMPCKNTEVETKLYFQPGKLGFDKVQRTD 420
Qy 421 SWDEYYTDPNPKPVPHOGGVIONTREYNNDDQRFAASRPDVNVYQTEPLTEDLTIVGPIK 480
Db 421 SWDEYYTDPNPKPVPHOGGVIONTREYNNDDQRFAASRPDVNVYQTEPLTEDLTIVGPIK 480
Qy 481 NFLKVSSSTGTDADYVVKLIDIVYQGKTMAGYQMMVRGEIMAGKYRNGFDKAQAL 540
Db 481 NFLKVSSSTGTDADYVVKLIDIVYQGKTMAGYQMMVRGEIMAGKYRNGFDKAQAL 540
Qy 541 TPGMVERVNEMPDVAHTFKKGHRIMYQVNQNSWPPLAERNPOVLAPYTAKADFRKATQ 600
Db 541 TPGMVERVNEMPDVAHTFKKGHRIMYQVNQNSWPPLAERNPOVLAPYTAKADFRKATQ 600
Qy 601 RIFHDVNNATYIEFSVLKD 619
Db 601 RIFHDVNNATYIEFSVLKD 619
Db 601 RIFHDVNNATYIEFSVLKD 619

RESULT 4
US-10-859-405-12
; Sequence 12, Application US/10859405
; Publication No. US20050032154A1
; GENERAL INFORMATION
; APPLICANT: YOKOZEKI, KENZO
; APPLICANT: SUZUKI, SONOKO
; APPLICANT: HARA, SEIICHI
; APPLICANT: ABE, ISAO
; TITLE OF INVENTION: METHOD FOR PRODUCING TRIPePTIDES AND/OR PEPTIDES LONGER THAN FILE REFERENCE: 254070050
; CURRENT FILING DATE: 2004-06-03
; PRIORITY APPLICATION NUMBER: US 10/859,405
; PRIORITY FILING DATE: 2003-08-01
; PRIORITY FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 12
; LENGTH: 619
; TYPE: PRT
; ORGANISM: Sphingobacterium sp.
; US-10-859-405-12

Query Match 100.0%; Score 3321; DB 5; Length 619;
Best Local Similarity 100.0%; Pred. No. 3.2e-260; Indels 0; Gaps 0;
Matches 619; Conservative 0; Mismatches 0; Deletions 0; Gaps 0;

Qy 1 MKNNTISCLTLAISOLHAQTAADSAYVRDHYEKTEVAPIMRDGKLLFTATYSPKDKSK 60
Db 1 MKNNTISCLTLAISOLHAQTAADSAYVRDHYEKTEVAPIMRDGKLLFTATYSPKDKSK 60
Db 61 KYPVLLNRTPTVTPYCGNEYKSLGNPQMMREGCYFVYQDVRGKMSSEGDFEDIRPTT 120
Db 61 KYPVLLNRTPTVTPYCGNEYKSLGNPQMMREGCYFVYQDVRGKMSSEGDFEDIRPTT 120
Qy 121 YSKDKKALDESTDTYDALEWLQKNLKNYNGRAGLYGSSYPGYSTGLVKTHPSLKAVSP 180
Db 121 YSKDKKALDESTDTYDALEWLQKNLKNYNGRAGLYGSSYPGYSTGLVKTHPSLKAVSP 180
Qy 181 QAPVTDMVYGDFFHHNGYLFLQDAFTFMSTFGVPRPKPITPQFKGK1QIKEADKYNFFA 240

Db 181 QAPVTDMVYGDFFHHNGYLFLQDAFTFMSTFGVPRPKPITPQFKGK1QIKEADKYNFFA 240
Qy 241 EAGTARELKEKYFGDSVQFWNDLFKHPDYDDENFKSRVITNSLQEVKPAVMVGGFPDAED 300
Db 241 EAGTARELKEKYFGDSVQFWNDLFKHPDYDDENFKSRVITNSLQEVKPAVMVGGFPDAED 300
Qy 301 AYGTFTKTVQSIEDKSCKNSILVAGPWHGGWTRAEGNYLGDQFEKTSITYQBQFQP 360
Db 301 AYGTFTKTVQSIEDKSCKNSILVAGPWHGGWTRAEGNYLGDQFEKTSITYQBQFQP 360
Qy 361 FPKXYLKDEGNFAPSEANIFVSSSNNEWHFBOMPCKNTEVETKLYFQPGKLGFDKVQRTD 420
Db 361 FPKXYLKDEGNFAPSEANIFVSSSNNEWHFBOMPCKNTEVETKLYFQPGKLGFDKVQRTD 420
Qy 421 SWDEYYTDPNPKPVPHOGGVIONTREYNNDDQRFAASRPDVNVYQTEPLTEDLTIVGPIK 480
Db 421 SWDEYYTDPNPKPVPHOGGVIONTREYNNDDQRFAASRPDVNVYQTEPLTEDLTIVGPIK 480
Qy 481 NFLKVSSSTGTDADYVVKLIDIVYQGKTMAGYQMMVRGEIMAGKYRNGFDKAQAL 540
Db 481 NFLKVSSSTGTDADYVVKLIDIVYQGKTMAGYQMMVRGEIMAGKYRNGFDKAQAL 540
Qy 541 TPGMVERVNEMPDVAHTFKKGHRIMYQVNQNSWPPLAERNPOVLAPYTAKADFRKATQ 600
Db 541 TPGMVERVNEMPDVAHTFKKGHRIMYQVNQNSWPPLAERNPOVLAPYTAKADFRKATQ 600
Qy 601 RIFHDVNNATYIEFSVLKD 619
Db 601 RIFHDVNNATYIEFSVLKD 619
Db 601 RIFHDVNNATYIEFSVLKD 619

RESULT 5
US-10-876-673-12
; Sequence 12, Application US/10876673
; Publication No. US0050124035A1
; GENERAL INFORMATION:
; APPLICANT: YOKOZEKI, KENZO
; APPLICANT: OHNO, AYAKO
; APPLICANT: HARA, SEIICHI
; APPLICANT: ABE, ISAO
; TITLE OF INVENTION: METHOD FOR PRODUCING ALPHA-L-ASPARTYL-L-PHENYLALANINE-BETA-ESTE.
; TITLE OF INVENTION: ALPHA-L-ASPARTYL-L-PHENYLALANINE-ALPHA-METHYL ESTER
; FILE REFERENCE: 254836US0PCT
; CURRENT FILING DATE: 2004-06-28
; PRIOR APPLICATION NUMBER: PCT/JP2004/000620
; PRIOR FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: JP 2003-016764
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: JP 2003-201819
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/491,546
; PRIOR FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 12
; LENGTH: 619
; TYPE: PRT
; ORGANISM: Sphingobacterium sp.
; US-10-876-673-12

Query Match 100.0%; Score 3321; DB 5; Length 619;
Best Local Similarity 100.0%; Pred. No. 3.2e-260;
Matches 619; Conservative 0; Mismatches 0; Deletions 0; Gaps 0;

Qy 1 MKNNTISCLTLAISOLHAQTAADSAYVRDHYEKTEVAPIMRDGKLLFTATYSPKDKSK 60
Db 1 MKNNTISCLTLAISOLHAQTAADSAYVRDHYEKTEVAPIMRDGKLLFTATYSPKDKSK 60
Qy 61 KYPVLLNRTPTVTPYCGNEYKSLGNPQMMREGCYFVYQDVRGKMSSEGDFEDIRPTT 120
Db 61 KYPVLLNRTPTVTPYCGNEYKSLGNPQMMREGCYFVYQDVRGKMSSEGDFEDIRPTT 120
Qy 121 YSKDKKALDESTDTYDALEWLQKNLKNYNGRAGLYGSSYPGYSTGLVKTHPSLKAVSP 180
Db 121 YSKDKKALDESTDTYDALEWLQKNLKNYNGRAGLYGSSYPGYSTGLVKTHPSLKAVSP 180
Qy 181 QAPVTDMVYGDFFHHNGYLFLQDAFTFMSTFGVPRPKPITPQFKGK1QIKEADKYNFFA 240

Qy 1 KYPVLLNRTPTVTPYCGNEYKSLGNPQMMREGCYFVYQDVRGKMSSEGDFEDIRPTT 120
Db 1 KYPVLLNRTPTVTPYCGNEYKSLGNPQMMREGCYFVYQDVRGKMSSEGDFEDIRPTT 120
Qy 61 KYPVLLNRTPTVTPYCGNEYKSLGNPQMMREGCYFVYQDVRGKMSSEGDFEDIRPTT 120
Db 61 KYPVLLNRTPTVTPYCGNEYKSLGNPQMMREGCYFVYQDVRGKMSSEGDFEDIRPTT 120

Db 61 KYPVLLNRTPTVSPYGGNEYKKSLGNPQMMREGYIFFYDVRGKWMSEGDFEDIRPTT 120
 Qy 121 YSKDKKAIDESTDTYDALEWLNQKNLKNYNGKAGIYLGYISYPGFYSTVGLVYKTHPSLKAASP 180
 Db 121 YSKDKKAIDESTDTYDALEWLNQKNLKNYNGKAGIYLGYISYPGFYSTVGLVYKTHPSLKAASP 180
 Db 181 QAPVTDMYIGDDFHNGVLFQDAFTMSTGVPRPKTPDQFCKQIQLKEADKYNFA 240
 Qy 181 QAPVTDMYIGDDFHNGVLFQDAFTMSTGVPRPKTPDQFCKQIQLKEADKYNFA 240
 Db 181 QAPVTDMYIGDDFHNGVLFQDAFTMSTGVPRPKTPDQFCKQIQLKEADKYNFA 240
 Qy 241 EAGTARBLKEKYFGDSVQFNDLFRKHPDYDDFWKSRSVITNSLOEYKPAVMVGFFDAED 300
 Db 241 EAGTARBLKEKYFGDSVQFNDLFRKHPDYDDFWKSRSVITNSLOEYKPAVMVGFFDAED 300
 Qy 241 EAGTARBLKEKYFGDSVQFNDLFRKHPDYDDFWKSRSVITNSLOEYKPAVMVGFFDAED 300
 Db 241 EAGTARBLKEKYFGDSVQFNDLFRKHPDYDDFWKSRSVITNSLOEYKPAVMVGFFDAED 300
 Qy 301 AYGTFKTYQSTEDKSCKNNSLVAGPWYHGGWRAEGNYLGDIQEPEKKTSITYQEQFQP 360
 Db 301 AYGTFKTYQSTEDKSCKNNSLVAGPWYHGGWRAEGNYLGDIQEPEKKTSITYQEQFQP 360
 Qy 361 PPKYKLDEGNPAPSEANIFYSGSNEMWKHFQWPKNVETKLYQPKQKLGFDVQRTD 420
 Db 361 PPKYKLDEGNPAPSEANIFYSGSNEMWKHFQWPKNVETKLYQPKQKLGFDVQRTD 420
 Qy 421 SWDEYYTDPNPKPVPHOGGIVQNRTREYMDORFAASRPDVNYCOTEPLTEDLTIVGPX 480
 Db 421 SWDEYYTDPNPKPVPHOGGIVQNRTREYMDORFAASRPDVNYCOTEPLTEDLTIVGPX 480
 Qy 421 SWDEYYTDPNPKPVPHOGGIVQNRTREYMDORFAASRPDVNYCOTEPLTEDLTIVGPX 480
 Db 421 SWDEYYTDPNPKPVPHOGGIVQNRTREYMDORFAASRPDVNYCOTEPLTEDLTIVGPX 480
 Qy 481 NFLKVSSSTGTDADYVVKLIDYVPPHOGGIVQNRTREYMDORFAASRPDVNYCOTEPLTEDLTIVGPX 540
 Db 481 NFLKVSSSTGTDADYVVKLIDYVPPHOGGIVQNRTREYMDORFAASRPDVNYCOTEPLTEDLTIVGPX 540
 Qy 541 TPGMVVKNFEMPDVHTFKKGHRIMVQVQNSWPLAERAPQVFLAPYTTAKDPRKATQ 600
 Db 541 TPGMVVKNFEMPDVHTFKKGHRIMVQVQNSWPLAERAPQVFLAPYTTAKDPRKATQ 600
 Qy 601 RIFHDVNNTAYIEFSVLKD 619
 Db 601 RIFHDVNNTAYIEFSVLKD 619
 Qy 601 RIFHDVNNTAYIEFSVLKD 619
 Db 601 RIFHDVNNTAYIEFSVLKD 619
 RESULT 6
 ; Sequence 20, Application US/11050829
 ; Publication No. US20050176150A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIRA, IKUO
 ; APPLICANT: YOKOZEKI, KENZO
 ; APPLICANT: SUZUKI, SONOKO
 ; APPLICANT: MIHARA, YASUHIRO
 ; APPLICANT: HIRAO, YOSHINORI
 ; TITLE OF INVENTION: SAME
 ; FILE REFERENCE: 265063US0
 ; CURRENT FILING DATE: 2005-02-07
 ; PRIOR APPLICATION NUMBER: US 60/617,060
 ; PRIOR FILING DATE: 2004-10-12
 ; PRIOR APPLICATION NUMBER: JP 2004-029844
 ; PRIOR FILING DATE: 2004-02-05
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: Patentin version 3.3
 ; SEQ ID NO 20
 ; LENGTH: 619
 ; TYPE: PRT
 ; ORGANISM: Sphingobacterium sp.
 ; US-11-050-829-20
 Query Match 100.0%; Score 3321; DB 6; Length 619;
 Best Local Similarity 100.0%; Pred. No. 3.2e-260; Indels 0; Gaps 0;
 Matches 619; Conservative 0; Mismatches 0; Insertions 0; Gaps 0;
 1 MKNTISCLTLALLSASQLQTAADSAYRDHYEKTEVALPMRDGKLLFTAIYSPDKSK 60
 1 MKNTISCLTLALLSASQLQTAADSAYRDHYEKTEVALPMRDGKLLFTAIYSPDKSK 60
 RESULT 7
 ; Sequence 6, Application US/10763179
 ; Publication No. US20040204577A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HARA, SEIICHI
 ; APPLICANT: YOKOZEKI, KENZO
 ; APPLICANT: TONOUCHI, ISAO
 ; APPLICANT: TONOUCHI, NACOTO
 ; APPLICANT: JOJIMA, YASURKO
 ; TITLE OF INVENTION: NOVEL PEPTIDE-FORMING ENZYME GENES
 ; FILE REFERENCE: 2478-BUS0
 ; CURRENT APPLICATION NUMBER: US/10/763,179
 ; CURRENT FILING DATE: 2004-01-26
 ; PRIOR APPLICATION NUMBER: JP 2003-16765
 ; PRIOR FILING DATE: 2003-01-24
 ; PRIOR APPLICATION NUMBER: US 60/491,612
 ; PRIOR FILING DATE: 2003-08-01
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 616
 ; TYPE: PRT
 ; ORGANISM: Empedobacter brevis
 ; US-10-763-179-6
 Query Match 66.2%; Score 2198.5; DB 4; Length 616;
 Best Local Similarity 64.3%; Pred. No. 3.3e-169;
 Matches 395; Conservative 85; Mismatches 129; Insertions 5; Gaps 2;
 5 ISCLTLALLSASQLQTAADSAYRDHYEKTEVALPMRDGKLLFTAIYSPDKSK 64
 Db

Db	8	VTLITLIGSTVGAQDAKADSAVDRNVEKTEQIVPMDGKLFATAIQPKDKTKTQPV	67	Qy	5	ISCLTIALLSASQLHQAQTAADSAYVRDHYEKTEVAIPMDGKLFATAIQSPDKSKKXCPV	64
Qy	65	LINRTPTVSPCQEYTKSLGNFPMRREGTIVYDVRGKMSDFEDIRPTYSKD	124	Db	8	VTLITLIGSTVGAQDAKADSAVDRNVEKTEQIVPMDGKLFATAIQPKDKTKTQPV	67
Db	68	LINRTPTVAPGVNEYTKSLGNFPMRREGTIVYDVRGKMSDFEDIRPTYSKD	127	Qy	65	LINRTPTVSPCQEYKKSLGNFPMRREGTIVYDVRGKMSDFEDIRPTYSKD	124
Qy	125	KKAIDESTDTDALEWLQNLKQNLKKNYNGKAGLYCISYPGFSYSTGLVKTPSLKAVSPQPV	184	Db	68	LINRTPTVAPGVNEYTKSLGNFPMRREGTIVYDVRGKMSDFEDIRPTYSKD	127
Db	128	KKAIDESTDTDALEWLQNLKQNLKKNYNGKAGLYCISYPGFSYSTMSLVNSHTPLKAVSPQPV	187	Qy	125	KKAIIDESTDTDALEWLQNLKQNLKKNYNGKAGLYCISYPGFSYSTMSLVNSHTPLKAVSPQPV	184
Qy	185	TDWYGDDFHNGVFLQDADFTMSTGVPKPXITPDQFKCKIQUIKEADKINFFAEGT	244	Db	128	KKAIIDESTDTDALEWLQNLKQNLKKNYNGKAGLYCISYPGFSYSTMSLVNSHTPLKAVSPQPV	187
Db	188	TNWFLGDDFHNGVFLINDSFPSMTFCVKRQFQITPDKGPKRFEPYKDNRYFA-SGS	246	Qy	185	TDWYGDDFHNGVFLQDADFTMSTGVPKPXITPDQFKCKIQUIKEADKINFFAEGT	244
Qy	245	ARELKBYFGDSVQFNNDLFKHPDQDFWKSRVITNSLOEYKPAVNWGGFPDAEDAYGT	304	Db	188	TNWFLGDDFHNGVFLINDSFPSMTFCVKRQFQITPDKGPKRFEPYKDNRYFA-SGS	246
Db	247	VRELKDKLQDNIKPFNDLFAFPDYDQWDRNVLPHLTNTQPAVNTVGGFDADYGA	306	Qy	245	ARELKBYFGDSVQFNNDLFKHPDQDFWKSRVITNSLOEYKPAVNWGGFPDAEDAYGT	304
Qy	305	FKTYQSLEDKSCKNNSTLVAGPKWYHGSWVRAESGNLYGDIQFERKTSITYQEOFQEPFFK	364	Db	247	VRELKDKLQDNIKPFNDLFAFPDYDQWDRNVLPHLTNTQPAVNTVGGFPDAEDAYGA	306
Db	307	FETYKATEKONPKATNTMVAGEFWHGSWVRSNGSTGDMQFASNTSEHYQOEIELFFNY	366	Qy	305	FKTYQSLEDKSCKNNSTLVAGPKWYHGSWVRAESGNLYGDIQFERKTSITYQEOFQEPFFK	364
Qy	365	YLKDEGNFAPSEANIFVGSMKQFWQPKVETKLYFOPOGKLGFDXVQRTDSWDE	424	Db	307	FETYKATEKONPKATNTMVAGEFWHGSWVRSNGSTGDMQFASNTSEHYQOEIELFFNY	366
Db	367	YLKDGNKPKRTPATITPGSNEWKQFWAQPKNVTTQKIVLQONGKIAFANKNTNTTDFE	426	Qy	365	YLKDEGNFAPSEANIFVGSMKQFWQPKVETKLYFOPOGKLGFDXVQRTDSWDE	424
Qy	425	YTDPNPKPVPHOGGVIONTRXYMDVORFALSRPDVWVQOBPLTEDLTIVGPXKFLK	484	Db	367	YLKDGNKPKRTPATITPGSNEWKQFWAQPKNVTTQKIVLQONGKIAFANKNTNTTDFE	426
Db	427	YVADPNSPVPSGGVLTRESRYMDQRFASTRDWVQSDILTEDTLAGPVINHLV	486	Qy	425	YTDPNPKPVPHOGGVIONTRXYMDVORFALSRPDVWVQOBPLTEDLTIVGPXKFLK	484
Qy	485	VSSGTGDDAYVVKLIDVYVNPDAASYQGKTMAGYQMMVGRFIMAGKYRNQGEDKAQALTPGM	544	Db	427	YVADPNSPVPSGGVLTRESRYMDQRFASTRDWVQSDILTEDTLAGPVINHLV	486
Db	487	VSTPTGTDADDVVKLIDVYVNPDAASYQGKTMAGYQMMVGRFIMAGKYRNQGEDKAQALTPGM	546	Qy	485	VSSGTGDDAYVVKLIDVYVNPDAASYQGKTMAGYQMMVGRFIMAGKYRNQGEDKAQALTPGM	544
Qy	545	VEKVNFMFDPDVAHTFKKGHRINVQVNSWFLPLAERNPQVFLAPYATKADPKATORIFH	604	Db	487	VSTPTGTDADDVVKLIDVYVNPDAASYQGKTMAGYQMMVGRFIMAGKYRNQGEDKAQALTPGM	546
Db	547	ETNVVTTMPDVGHTFKGHRIMIQVNSWFLPLAERNPQFNMVYEATSVDLKQTQIYH	606	Qy	545	VEKVNFMFDPDVAHTFKKGHRINVQVNSWFLPLAERNPQFNMVYEATSVDLKQTQIYH	604
Qy	605	DYNNATYIEPSVLIK	618	Db	547	ETNVVTTMPDVGHTFKGHRIMIQVNSWFLPLAERNPQFNMVYEATSVDLKQTQIYH	606
Db	607	---TSIEIIPVLIK	616	Qy	605	DYNNATYIEPSVLIK	618
Db	607	---TSIEIIPVLIK	616	Db	607	---TSIEIIPVLIK	616
RESULT 8							
US-10-849-814-6							
; Sequence 6, Application US/10849814							
; Publication No. US20040219631A1							
; GENERAL INFORMATION							
; APPLICANT: YOKOZEKI, KENZO							
; APPLICANT: SUZUKI, SONOKO							
; APPLICANT: HARA, SEIICHI							
; APPLICANT: ABE, ISAO							
; TITLE OF INVENTION: METHOD FOR PRODUCING TRIPETIDES AND/OR PEPTIDES LONGER THAN TRIPETIDES							
; FILE REFERENCE: 252308050CONT							
; CURRENT APPLICATION NUMBER: US/10/849-814							
; CURRENT FILING DATE: 2004-05-21							
; PRIOR APPLICATION NUMBER: PCT/JP03/09466							
; PRIOR FILING DATE: 2003-07-25							
; NUMBER OF SEQ ID NOS: 14							
; SOFTWARE: PatentIn version 3.1							
; SEQ ID NO: 6							
; LENGTH: 616							
; TYPE: PRT							
; ORGANISM: Empedobacter brevis							
; US-10-849-814-6							
; LENGTH: 616							
; TYPE: PRT							
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; US-10-849-814-6							
; LENGTH: 616							
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; ORGANISM: Empedobacter brevis							
; US-10-849-814-6							
; LENGTH: 616							
; TYPE: PRT							
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; US-10-849-814-6							
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; ORGANISM: Empedobacter brevis							
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; TYPE: PRT							
; ORGANISM: Empedobacter brevis							
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US-10-859-405-6									
Query Match Score	66.2%	DB 5;	Length 616;						
Best Local Similarity	64.3%	Pred. No.	3.3e-169;						
Matches 395;	Conservative	85;	Mismatches	129;	Indels	5;	Gaps	2;	
5 ISCLTLIALSASQLHQATAADSAVYRDHYETKEVALIPMRDGKFLTAIYSPRDKSKCKPV 64									
8 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	Qy	5 ISCLTLIALSASQLHQATAADSAVYRDHYETKEVALIPMRDGKFLTAIYSPRDKSKCKPV 64	Query Match Score	66.2%	DB 5;	Length 616;			
65 LLNRTPYTSPYGONEYKKSGLNPFQMREGYIFYQDVRGKWMSEGDFEDIRPITYSKD 124	Db	64 Best Local Similarity 64.3%; Pred. No. 3.3e-169; Mismatches 85; Indels 129; Gaps 5;	Local Similarity	64.3%;	Pred. No. 3.3e-169;				
68 LLNRTPYTSPYGONEYKKSGLNPFQMREGYIFYQDVRGKWMSEGDFEDIRPITYSKD 124	Qy	5 ISCLTLIALSASQLHQATAADSAVYRDHYETKEVALIPMRDGKFLTAIYSPRDKSKCKPV 64	Matches 395;	Conservative	85;	Mismatches	129;	Indels	5;
125 KKAIDESTDTYDALEWLQNLKNTKNGAGLYGISTPGFYSTVGLYTHPSLKLAVSQAPV 184	Db	65 LLNRTPYTSPYGONEYKKSGLNPFQMREGYIFYQDVRGKWMSEGDFEDIRPITYSKD 124	Score 2198.5;	DB 5;	Length 616;				
128 KKAIDESTDTFDTLEMILAKNLKNTKKGAGLYGISTPGFYSTMSLVLNSHPTLKAVSQAPV 187	Qy	65 LLNRTPYTSPYGONEYKKSGLNPFQMREGYIFYQDVRGKWMSEGDFEDIRPITYSKD 124	Sequence 6, Application US/10876673						
185 TDWYIGDDFHNGVLFQLODAFTFMSTFGVPRPKPITPDQPKGKIQ1KEADKYNFFAEAGT 244	Db	66 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	Publication No. US20050124035A1						
188 TNWFUGDDFHNGVLFPLNDSSFSMTPFGVGRPQTPDQPKRFEPIKDNYRFA-SGS 246	Qy	67 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	GENERAL INFORMATION:						
245 ARELKEKYFGDSVQFNNDLFKHPDYDFDWFSRVITNSLQEYKPAVMVGGFPDAEADAYGT 304	Db	68 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	APPLICANT: YOKOZEKI, KENZO						
247 VKELDKYLQDNKTYNDLPAHPDQDFWQDRNVLPHLTNVQPAVMVGGFPDAEADYVA 306	Qy	69 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	APPLICANT: OHNO, AYAKO						
305 FKTVOSEDGSKKNSILVAGPWTGGWVRAEGNLYLQD1QPEKKNSITYQEQEOPFKY 364	Db	70 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	APPLICANT: HARA, SEIICHI						
307 FETYKAIEKONPKATNIMMAGPWFGGWVRSNGSTFGDMQFASNTSEHYYQOBIELPFFNY 366	Qy	71 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	APPLICANT: ABE, ISAO						
365 YLDEGNNFAPEANIFVSGSNNEWKHFEEQWPKNVETKLYFQPOQKLGFDKVQRTDSWDE 424	Db	72 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	APPLICANT: TSVENINMPDVYQTEPLTEDLTIVSPKNEFLK 484						
367 YLQDGKGNFKPTEATIFTGSGNEWKHFEEQWPKNVETKLYFQPOQKLGFDKVQRTDSWDE 426	Qy	73 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	APPLICANT: YUARDENFAPSZANIFVSGSNNEWKHFEEQWPKNVETKLYFQPOQKLGFDKVQRTDSWDE 424						
425 YVTDPBNKPVPHQGGVQIQRNTREMYDDORPFAASRPDVMMYQTEPLTEDLTIVGP1KPNFLK 484	Db	74 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	APPLICANT: YUADENSPVPSGGVLETTRSREMYDDORPFASTRPDVMMYQSDILTEDLTLAGPV1NHLY 486						
427 YVADENSPVPSGGVLETTRSREMYDDORPFASTRPDVMMYQSDILTEDLTLAGPV1NHLY 486	Qy	75 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	APPLICANT: YVADENSPVPSGGVLETTRSREMYDDORPFASTRPDVMMYQSDILTEDLTLAGPV1NHLY 486						
485 VSSTGTDADYVVKLIDVYPNDAASTYQGKTNAGYQMVREGEIMAGKYRNGFDKAQALTPGM 544	Db	76 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	APPLICANT: YSSTGTDADYVVKLIDVYPNDAASTYQGKTNAGYQMVREGEIMAGKYRNGFDKAQALTPGM 544						
487 VSTGTDADYVVKLIDVYPENTPKPNKLNAGYQNLIRAT1MKGYRNSNSNPAMVPK 546	Qy	77 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	APPLICANT: YSSTGTDADYVVKLIDVYPENTPKPNKLNAGYQNLIRAT1MKGYRNSNSNPAMVPK 546						
545 VEKYNFEMPDDVAAHTPKKGHRIMYVONWSNPPLAERNPQVFLAPYPTKADFRKATOR1FH 604	Db	78 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	APPLICANT: VEKYNFEMPDDVAAHTPKKGHRIMYVONWSNPPLAERNPQVFLAPYPTKADFRKATOR1FH 604						
547 BTNTVTTMPDVGHTPKGHRIMIQVNQNSWFLPLADRNPNQPMVNEYATSQDYLKQTQRYH 606	Qy	79 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	APPLICANT: BTNTVTTMPDVGHTPKGHRIMIQVNQNSWFLPLADRNPNQPMVNEYATSQDYLKQTQRYH 606						
605 DVNNATYIERSVULK 618	Db	80 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	APPLICANT: DVNNATYIERSVULK 618						
607 ---TSVIB1PVLK 616	Qy	81 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	APPLICANT: ---TSVIB1PVLK 616						
ULT 10		82 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	APPLICANT: ABE, ISAO						
10-859-405-6		83 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	APPLICANT: METHOD FOR PRODUCING ALPHA-L-ASPARTYL-L-PHENYLALANINE						
SEQUENCE 6, Application US/10859405		84 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	SEQUENCE 6, Application US/10876673						
BENEFICIAL INFORMATION:		85 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	BENEFICIAL INFORMATION: AND METHOD FOR PRODUCING ALPHA-L-ASPARTYL-L-PHENYLALANINE - ALPHA-METHYL ESTER						
APPLICANT: YOKOZEKI, KENZO		86 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	APPLICANT: YOKOZEKI, KENZO						
APPLICANT: SUZUKI, SONOKO		87 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	APPLICANT: OHNO, AYAKO						
APPLICANT: HARA, SEIICHI		88 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	APPLICANT: HARA, SEIICHI						
APPLICANT: ABE, ISAO		89 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	APPLICANT: ABE, ISAO						
TITLE OF INVENTION: METHOD FOR PRODUCING TRIPETIDES		90 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	TITLE OF INVENTION: METHOD FOR PRODUCING ALPHA-L-ASPARTYL-L-PHENYLALANINE						
FILE REFERENCE: 2547070US0		91 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	FILE REFERENCE: 2547070US0						
CURRENT APPLICATION NUMBER: US/10/859,405		92 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	CURRENT APPLICATION NUMBER: US/10/859,405						
CURRENT FILING DATE: 2004-06-13		93 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	CURRENT FILING DATE: 2004-06-13						
PRIOR APPLICATION NUMBER: US 60/491,547		94 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	PRIOR APPLICATION NUMBER: US 60/491,547						
PRIOR FILING DATE: 2003-08-01		95 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	PRIOR FILING DATE: 2003-08-01						
PRIOR APPLICATION NUMBER: JP 2002-218958		96 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	PRIOR APPLICATION NUMBER: JP 2002-218958						
NUMBER OF SEQ ID NOS: 21		97 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	NUMBER OF SEQ ID NOS: 21						
PATENT IN version 3.3		98 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	PATENT IN version 3.3						
PBQ ID NO 6		99 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	PBQ ID NO 6						
LENGTH: 616		100 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	LENGTH: 616						
ORGANISM: Empedobacter brevis		101 VTLTLLLGSTVGAODAKADSAYVEDNIEKIEQVTPMDGKFLTAIYQPRDKTKQYPV 67	ORGANISM: Empedobacter brevis						

PRIOR FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 6
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Empedobacter brevis
; US-10-876-673-6

Query Match Score 2198.5; DB 5; Length 616;
Best Local Similarity 64.3%; Pred. No. 3.3e-169;
Matches 395; Conservative 85; Mismatches 129; Indels 5; Gaps 2;
Query Match Score 2198.5; DB 6; Length 616;
Best Local Similarity 64.3%; Pred. No. 3.3e-169;
Matches 395; Conservative 85; Mismatches 129; Indels 5; Gaps 2;
; ORGANISM: Empedobacter brevis
; US-11-050-829-14

Qy 5 ISCLTLALLSASQLHQATTAADSAYRDHYBKTTEVAIPMRDGGKLFATAISPKDKSKKKYPV 64
Db 8 VTTLLTLLGSTVGFAODAKADSAYRDNYECKIEQVTPMDGDTKLFLTAIYOPRDKTKQYPV 67

Qy 65 LLNRTPTVSPYQNEYKSLGNPOMMREGYIIFTYDVRGKWMSEGDFDIRPTYSKD 124
Db 68 LLNRTPTVSPYQNEYKSLGNPFTMRESFIVYQDRGKWMSEGDFDIRPTYSKD 127

Qy 125 KRAIDESTDYYDALEWLQNLKNTKAGLYISPGFYSTVGLYRTHPSLKAVALSQAPV 184
Db 128 KRAIDESTDYYDALEWLQNLKNTKAGLYISPGFYSTVGLYRTHPSLKAVALSQAPV 187

Qy 185 TDWYIGDDPHENGVLFLQADTFMSNFGVPRPKPTIDPOFGKQ1QIKEADKYNFFAEGST 244
Db 188 TNWFLGDDPHENGVLFLQADTFMSNFGVPRPKPTIDPOFGKQ1QIKEADKYNFFAEGST 246

Qy 245 ARELKVKYFGDSVQFTNDLKFHPDQDFWKSRSVITNSLQEVYKPAVNVGFFDAEDAYGT 304
Db 247 VKELODKYLDQNKIFYKNDLFAHPDQDFWKSRSVITNSLQEVYKPAVNVGFFDAEDAYGT 306

Qy 305 FKYQSIEDKSKKNNSTLVAGEWYHCGWVRAEGLNTLGDIQFCKTSITYDEQFEOPFKY 364
Db 307 FETYKAIEBKQPKPATNMVAGFWHCGWVRSNGSTFGDMQFASNTSEHYYQEIELPFNY 366

Qy 365 YLKDEBNAPSBANIFVGSNSNEWKHEPQWPKNVETKCKLYFQPOQKLGDFKQVORTSDNDE 424
Db 367 YLKDEBNAPSBANIFVGSNSNEWKHEPQWPKNVETKCKLYFQPOQKLGDFKQVORTSDNDE 426

Qy 425 YTDPNPKVPHQGGVQNRTEYMDQRFQASRPDVMTQTEPLTDLTVPIKNFLK 484
Db 427 YVADPNSPVPYSGGVLETSSREYMDQRFQASRPDVMTQTEPLTDLTVPIKNFLK 486

Qy 485 VSSTGTDADYVVLKLIDVYPPNDAASYQCKTMVQYQMVREGEIMAGCYRNFGDKAQALTPGM 544
Db 487 VSSTGTDADYVVLKLIDVYPPNDAASYQCKTMVQYQMVREGEIMAGCYRNFGDKAQALTPGM 546

Qy 545 VEKVNPEMPDVAYHTPKKGHRIMQVQNSWPLAERNPQVFLAPYATKAFRKATORIFH 604
Db 547 ETNVTTMPDVGHTFKKGHRIMQVQNSWPLAERNPQVFLAPYATKAFRKATORIFH 606

Qy 605 DVNNATYIBPSVLIK 618
Db 607 ---TSYBIPVLIK 616

RESULT 12
US-11-050-829-14
; Sequence 14, Application US/11050829
; GENERAL INFORMATION:
; Publication No. US20050176150A1
; APPLICANT: KIRA, IKUO
; APPLICANT: YOKOZEKI, KENZO
; APPLICANT: SUZUKI, SONOKO
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: HIRAO, YOSHINORI
; TITLE OF INVENTION: MUTANT MICROORGANISM AND METHOD FOR PRODUCING PEPTIDE USING THE
; TITLE OF INVENTION: MUTANT MICROORGANISM AND METHOD FOR PRODUCING PEPTIDE USING THE
; FILE REFERENCE: 268256US0
; CURRENT APPLICATION NUMBER: US/11/050,829
; CURRENT FILING DATE: 2005-02-07

; PRIOR APPLICATION NUMBER: US 60/617,060
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: JP 2004-029844
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 14
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Empedobacter brevis
; US-11-050-829-14

Query Match Score 2198.5; DB 5; Length 616;
Best Local Similarity 64.3%; Pred. No. 3.3e-169;
Matches 395; Conservative 85; Mismatches 129; Indels 5; Gaps 2;
Query Match Score 2198.5; DB 6; Length 616;
Best Local Similarity 64.3%; Pred. No. 3.3e-169;
Matches 395; Conservative 85; Mismatches 129; Indels 5; Gaps 2;
; ORGANISM: Empedobacter brevis
; US-11-050-829-14

Qy 5 ISCLTLALLSASQLHQATTAADSAYRDHYBKTTEVAIPMRDGGKLFATAISPKDKSKKKYPV 64
Db 8 VTTLLTLLGSTVGFAODAKADSAYRDNYECKIEQVTPMDGDTKLFLTAIYOPRDKTKQYPV 67

Qy 65 LLNRTPTVSPYQNEYKSLGNPOMMREGYIIFTYDVRGKWMSEGDFDIRPTYSKD 124
Db 68 LLNRTPTVSPYQNEYKSLGNPFTMRESFIVYQDRGKWMSEGDFDIRPTYSKD 127

Qy 125 KRAIDESTDYYDALEWLQNLKNTKAGLYISPGFYSTVGLYRTHPSLKAVALSQAPV 184
Db 128 KRAIDESTDYYDALEWLQNLKNTKAGLYISPGFYSTVGLYRTHPSLKAVALSQAPV 187

Qy 185 TDWYIGDDPHENGVLFLQADTFMSNFGVPRPKPTIDPOFGKQ1QIKEADKYNFFAEGST 244
Db 188 TNWFLGDDPHENGVLFLQADTFMSNFGVPRPKPTIDPOFGKQ1QIKEADKYNFFAEGST 246

Qy 245 ARELKVKYFGDSVQFTNDLKFHPDQDFWKSRSVITNSLQEVYKPAVNVGFFDAEDAYGT 304
Db 247 VKELODKYLDQNKIFYKNDLFAHPDQDFWKSRSVITNSLQEVYKPAVNVGFFDAEDAYGT 306

Qy 305 FKYQSIEDKSKKNNSTLVAGEWYHCGWVRAEGLNTLGDIQFCKTSITYDEQFEOPFKY 364
Db 307 FETYKAIEBKQPKPATNMVAGFWHCGWVRSNGSTFGDMQFASNTSEHYYQEIELPFNY 366

Qy 365 YLKDEBNAPSBANIFVGSNSNEWKHEPQWPKNVETKCKLYFQPOQKLGDFKQVORTSDNDE 424
Db 367 YLKDEBNAPSBANIFVGSNSNEWKHEPQWPKNVETKCKLYFQPOQKLGDFKQVORTSDNDE 426

Qy 425 YTDPNPKVPHQGGVQNRTEYMDQRFQASRPDVMTQTEPLTDLTVPIKNFLK 484
Db 427 YVADPNSPVPYSGGVLETSSREYMDQRFQASRPDVMTQTEPLTDLTVPIKNFLK 486

Qy 485 VSSTGTDADYVVLKLIDVYPPNDAASYQCKTMVQYQMVREGEIMAGCYRNFGDKAQALTPGM 544
Db 487 VSSTGTDADYVVLKLIDVYPPNDAASYQCKTMVQYQMVREGEIMAGCYRNFGDKAQALTPGM 546

Qy 545 VEKVNPEMPDVAYHTPKKGHRIMQVQNSWPLAERNPQVFLAPYATKAFRKATORIFH 604
Db 547 ETNVTTMPDVGHTFKKGHRIMQVQNSWPLAERNPQVFLAPYATKAFRKATORIFH 606

Qy 605 DVNNATYIBPSVLIK 618
Db 607 ---TSYBIPVLIK 616

RESULT 13
US-11-085-576-12
; Sequence 12, Application US/11085576
; Publication No. US20050227325A1
; GENERAL INFORMATION:
; APPLICANT: HIRAO, YOSHINORI
; TITLE OF INVENTION: RECOMBINANT POLYNUCLEOTIDE
; FILE REFERENCE: 268256US0
; CURRENT APPLICATION NUMBER: US/11/085,576
; CURRENT FILING DATE: 2005-03-22
; PRIOR APPLICATION NUMBER: JP 2004-083481

PRIOR FILING DATE: 2004-03-22
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 12
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Empedobacter brevis
US-11-085-576-12

Query Match Score 2198.5; DB 6; Length 616;
Best Local Similarity 64.3%; Pred. No. 3.3e-169;
Matches 395; Conservative 85; Mismatches 129; Indels 5; Gaps 2;

Qy 5 ISCLTIALSASQLHQAQTADSAVYRDHYTEVAIPMRDGSKKLUFTAIYSPKDKSKKYPV 64
Db 8 VITLILLGSTVGAQDAKASAYRDHYTEVAIPMRDGSKKLUFTAIYSPKDKSKKYPV 67
Qy 65 LLNRTPTVSPYGNEYKSLGNFPQMMREGYIFYQDVRGKMMSEGDDFDIRPTTYSKD 124
Db 68 LLNRTPTVSPYGNEYKSLGNFPTEMMREGFYQDVRGKMMSEGEEFDVRPINPSKS 127
Qy 125 KKAIDESTDTYDALETLQKLNKNTYNGKAGLYGISTPGFVITYVGLVTHPULKAVSQAQPV 184
Db 128 KKAIDESTDTDTELETLQKLNKNTYNGKAGLYGISTPGFVITYVGLVTHPULKAVSQAQPV 187
Qy 185 TDWYIGDDFHNGVLFQDAFTTEMSTFGVPRPKITPDQFKGKQIKEADKYNFFAEAQT 244
Db 188 TNWFLDDFHNGVLFINDTSISFTGMPKPRKFYPIKONYRFTA-SGS 246
Qy 245 ARELKELYFGDSVQFWNDLFKHPDYDDFWKSRVITNSLQEYVKPAWMVYGGFFDAEDAYST 304
Db 247 VKEKDXKLQDNKIEKFNDFLAFHAPDQFWDNVLPHLTNVQPAWMVYGGFFDAEDVYGA 306
Qy 305 FKTQSYIEDRSKKNNSILVACGPWTFGGWVRAEAGNYLGDLOPEKTSITYKOBQFOPPFY 364
Db 307 FETYKAIEKQNPKATNMVGAVPWFICGWVPSNSNGTFSQDQFASNTSEHITQOEIELPFPNY 366
Qy 365 YLDEGENFAPSBEANIFVGSGNEWKHFQWNPKNVETKLYFQPOQSKLGFDFKVQRTDSMDS 424
Db 367 YLKDRCNFKPTEATPITGSNEWKQDAWPKNVTQKYLQONGKIANKNTNTTTFDE 426
Qy 425 YVTDPNKPVPHOGGYQNTRTREYMDQRFPAASRPDVMMYQTEPLDTIVGPIKNIPLK 484
Db 427 YVADPNSPVPSGGVLETRSREYMDQRFASPRDVMMYQSDLITEDTLAGPVINHLV 486
Qy 485 VSSTGTDADYVVKLDVYPPNDAASYQGKTMAGYOMVREGRIMAGKTYRNQGDKAQALTPGM 544
Db 487 VSTGTDADYVVKLDVYPPNDAASYQGKTMAGYOMVREGRIMAGKTYRNQGDKAQALTPGM 546
Qy 545 VEKVNPEMPDVAVHTFKGHRIMVOVNSWPLABERNPQVPLAPTTAKDFAKTAQRIPH 604
Db 547 ETNVTTYMPDVGHTFKGGHRIMIQVQNSWFLADRNPPQFMNTYEATSQDYLKQTQIYH 606
Qy 605 DVNNNATYIEFSVLIK 618
Db 607 ---TSYIEFPLVK 616

RESULT 14
US-11-085-576-3
Sequence 3, Application US/11085576
GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: HIRAO, YOSHINORI
; TITLE OF INVENTION: RECOMBINANT POLYNUCLEOTIDE
; FILE REFERENCE: 268258US0
; CURRENT APPLICATION NUMBER: US/11/085,576
; PRIOR APPLICATION NUMBER: JP 2004-083481
; CURRENT FILING DATE: 2005-03-22
; PRIOR FILING DATE: 2004-03-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 18
; LENGTH: 625

Query Match Score 2187.5; DB 6; Length 594;
Best Local Similarity 65.5%; Pred. No. 2.4e-168;
Matches 390; Conservative 83; Mismatches 117; Indels 5; Gaps 2;

Qy 24 ADSAIVRDHYEKTEVAIPMRDGKLUFTAIYSPKDKSKKYPVLIQRTPTVSPYGCNEYKK 83
Db 5 ADSAIVRDHYEKTEVAIPMRDGKLUFTAIYSPKDKSKKYPVLIQRTPTVSPYGCNEYKK 64
Qy 84 SIGNPQMREGYIFYQDVRGKMMSEGDDFDIRPTTYSKDKAIDESTDTYDALEWLQK 143
Db 65 SLGNPPTEMREGFIVYQDVRGKMMSEGEEFDVREINPSKSKAIDESTDTFDTLWMLAK 124
Qy 144 NLRNTRKAGLYGISTPGFVITYVGLVTHPULKAVSQAQPVTDWYIGDDFHNGVLFQD 203
Db 125 NLRNTRKAGLYGISTPGFVITYVGLVTHPULKAVSQAQPVTDWYIGDDFHNGVLFQD 184
Qy 204 AFTMISTFGVYPRPKITPDQFKGKQIKEADKTNFQAFATEARELKELYFGDSVOPWNDL 263
Db 185 SPSFNFPGVYKRPQITPDQGPKRREBYPKDNTRYA-SSSVKEKDXKLQDNKIKFYNDL 243
Qy 264 EKHPPYDDEWSKRVITNSLQEYVKDQAMVWJGGEFDLDAIGTEKTYOSIDSKSKNNSILV 323
Db 244 FAHPYDQFWQDRNLPHLTNVQPAWMVYGGFFDAEDVYGAETFYKAEKQNPKATNIMV 303
Qy 324 AGPWTGGWVRAEAGNYLGDLOFEKTSITQFFQPFKYLKDEGNFAPSEANI.FVSG 383
Db 304 AGPWTGGWVRAEAGNYLGDLOFEKTSITQFFQPFKYLKDEGNFAPSEANI.FVSG 363
Qy 384 SNEWHFEQMPKVNTEKLYFOPQGKLGFDKVQRTDSWEYVTDPNKPVPHOCGIVNQ 443
Db 364 SNEWHFEQMPKVNTEKLYFOPQGKLGFDKVQRTDSWEYVTDPNKPVPHOCGIVNQ 423
Qy 444 TREVYVNDQFRAASPDVWVYQCEPLTELTIVGPKNLKVSSGTGTDADYVVKLIDVYP 503
Db 424 SREYVNDQFRAASPDVWVYQSDLITEDTLAGPVINHLVSTGTDADYVVKLIDVYP 483
Qy 504 NDAASYQGKTMAGYQNLIAEIMGKYSRFSNEAMVNPKETTYMPDVGHTFKKGH 563
Db 484 ENTPEKKNLMAQNLIAEIMGKYSRFSNEAMVNPKETTYMPDVGHTFKKGH 543
Qy 564 RIMVYQNSWFLAERNPQVFLAYTATADFRKATORIYHIFHDYNATYIEFSVLIK 618
Db 544 RIMVYQNSWFLAERNPQOVMNTYEATSKDYLKQTQIYH---TSYIEFPLVK 594

RESULT 15
US-10-76-179-18
Sequence 18, Application US/10763179
; Publication No. US20040204577A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: NOVEL PEPTIDE-FORMING ENZYME GENES
; FILE REFERENCE: 247848US0
; CURRENT APPLICATION NUMBER: US/10/763,179
; PRIORITY FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: JP 2003-16765
; PRIORITY FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: US 60/491,612
; PRIORITY FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 18
; LENGTH: 625

TYPE: PRT
 ORGANISM: Pedobacter heparinus
 US-10-763-179-18

Query Match Score 2081; DB 4; Length 625;
 Best Local Similarity 61.8%; Pred. No. 1.1e-159;
 Matches 383; Conservative 81; Mismatches 150; Index 6; Gaps 3;

4 TISCLTALLSSQHQAATADSAYVDRHYETEVAIPMRDGKLETTAISPKDKSKKKYK 63
 6 SFSPFLPLFPLTSLASAQ-QSDSAYITRONTYKIERLIPMRCGKLFATAIYPKDTSKKYK 64

64 VILLNRTPTVSPYQGQNEYIKSLSGNPOMMRGKMMSEGDFEDIRPTYSK 123
 65 FMLNRTPYTVSPYGENNYKTSGLSPSLPIKEGPIFYQDVKGKMSSEGKFEDVRPOIAK 124

Qy 124 DKKA-IDESTDPTYDALEWLQKNLKNTNGKAGLYISYPGPYSTVGUVKTHPSLKAVSPQA 182
 Db 125 KRKTIDDBSSDTYDIDWLRLNTPIGNNRKTRGTYISYPGPYATAALPDAPSLKAVSPQA 184

Qy 183 PYTDWYIGDDFHANGULFLQDAFTENSTMFGYPRPKTIPDQFGKQIQLKEADKYNFFAA 242
 Db 185 PYTDWTFGDDFHANGULFLADIFSFYTFGVPKPITPDRKPKPDFPVKDNTREFEL 244

Qy 243 GTAREJKEYFGDSVQFDNLFKHPDYDEWKSRRVITNSLOEVKPAVMYGGFPDAEDAY 302
 Db 245 GPLKNITKRYGDTIREWINDNAHTNDAFWKARNNTPHLGVKPAVLVGGFPDAEDLY 304

Qy 303 GTFKTYOSIEDKSKKKNSILYAGPWTYHGGMVRAEGNYLGDQFEKKTSTYQEQQEOPFFF 362
 Db 305 GTLKTYQAIEKONPSSRNLYMGPWTYHGWARSTGSFPGDINFQOPTTSYQONYBFPPF 364

Qy 363 KYLLDEGNNPAPSEANIFVCSNEWKHFQKPPKVNTEKLYFPOQGKLGPDKVQRTDSW 422
 Db 365 MQYLKEAAPAKIAEATIFTITGSNEWKFKSSMPPQDTEERTLYLQPNQKLSPEKVQRTDSW 424

Qy 423 DEYVTDENKPVYKLVLDYYPND---AASYGKTMAGKOMMVRGEIMACKYRNGFDKAQ 538
 Db 425 DEYVSDENSPPIPYQDGQTQTSREIMIDQRFASRPRDPVRFQTEBLSSDTLTGPVLA 484

Qy 483 LKVSSTGTDADYVVKLIDYYPND---AASYGKTMAGKOMMVRGEIMACKYRNGFDKAQ 538
 Db 485 LVVSTTGTDADYVVKLIDYYPDTPNPVPNPKNLIMGGYQMLVRGEIMACKYRNSFEKE 544

Qy 539 ALTPGMVYKVNPFEMPDVATPKKGHRIMVQYQNSWPLAERNPOVFLAPPATKADFRKA 598
 Db 545 BFVPGTITKVNALPDVATPKKGHRIMIQQNSWPLAERNPOQFMIDYQAEPCSDFRKA 604

Qy 599 TQRIFDVANNATYIEPSVLK 618
 Db 605 THRIFDVAHNASAITVNLK 624

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OM nucleic - nucleic search, using sw model

Run on: January 21, 2006, 15:45:47 ; Search time 1582.12 Seconds
(without alignments)

10113.830 Million cell updates/sec

Title: US-10-849-814-11

Perfect score: 1 gaaaccaaatgttaaaaatt.....attacgaggtaaatcggaa 1935

Sequence: 979352 seqs, 413468905 residues

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA_Main:
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2: /cgn2_6/ptodata/1/pubna/US08_PUBCOMB.seq;
3: /cgn2_6/ptodata/1/pubna/US09A_PUBCOMB.seq;
4: /cgn2_6/ptodata/1/pubna/US10A_PUBCOMB.seq;
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9: /cgn2_6/ptodata/1/pubna/US10F_PUBCOMB.seq;
10: /cgn2_6/ptodata/1/pubna/US11_FUBCOMB.seq;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description	
1	1935	100.0	1935	8	US-10-763-179-11	<i>Aba</i>	
2	1935	100.0	1935	8	US-10-814-11	<i>ay</i>	
3	1935	100.0	1935	8	US-10-855-533-11	<i>ay</i>	
4	1935	100.0	1935	8	US-10-855-405-11	<i>ay</i>	
5	1935	100.0	1935	9	US-10-876-673-11	<i>ay</i>	
6	1935	100.0	1935	10	US-11-050-829-19	<i>ay</i>	
7	771	39.8	2024	8	US-10-763-179-5	<i>ay</i>	
8	771	39.8	2024	8	US-10-844-814-5	<i>ay</i>	
9	771	39.8	2024	8	US-10-855-533-17	<i>ay</i>	
10	771	39.8	2024	8	US-10-855-405-5	<i>ay</i>	
11	771	39.8	2024	9	US-10-876-673-5	<i>ay</i>	
12	771	39.8	2024	10	US-11-050-829-13	<i>ay</i>	
13	771	39.8	2024	10	US-11-055-576-11	<i>ay</i>	
14	694.6	35.9	1974	8	US-10-763-179-17	<i>ay</i>	
15	694.6	35.9	1974	8	US-10-855-533-17	<i>ay</i>	
16	694.6	35.9	1974	9	US-10-876-673-17	<i>ay</i>	
17	368.4	19.0	2018	8	US-10-763-179-22	<i>ay</i>	
18	368.4	19.0	2018	8	US-10-855-533-22	<i>ay</i>	
19	368.4	19.0	2018	9	US-10-876-673-22	<i>ay</i>	
20	332	17.2	1931	8	US-10-763-179-24	<i>ay</i>	
21	332	17.2	1931	8	US-10-855-533-24	<i>ay</i>	
22	332	17.2	1931	9	US-10-876-673-24	<i>ay</i>	
23	277	14.3	2036	8	US-10-855-533-26	<i>ay</i>	
24	277	14.3	2036	9	US-10-876-673-26	<i>ay</i>	
c	26	119.8	2.9	3011208	7	US-10-398-221-9	<i>ay</i>
c	27	55.8	2.9	2252	7	US-10-398-221-1912	<i>ay</i>
c	28	55.8	2.6	2888	7	US-10-398-221-3677	<i>ay</i>
c	29	50.4	2.6	632	8	US-10-377-930-5211	<i>ay</i>
c	30	44.4	2.3	426	6	US-10-349-680-135	<i>ay</i>
c	31	43.4	2.2	6498	9	US-10-459-352A-45	<i>ay</i>
c	32	43.4	2.2	7268	9	US-10-459-352A-33	<i>ay</i>
c	33	41.8	2.2	7951	9	US-10-459-352A-43	<i>ay</i>
c	34	41.8	2.2	9480	9	US-10-459-352A-27	<i>ay</i>
c	35	41.8	2.2	9954	9	US-10-459-352A-42	<i>ay</i>
c	36	41.8	2.2	15613	9	US-10-459-352A-23	<i>ay</i>
c	37	41.8	2.2	16309	9	US-10-459-352A-24	<i>ay</i>
c	38	41.8	2.2	16387	9	US-10-459-352A-25	<i>ay</i>
c	39	41.8	2.2	16854	9	US-10-459-352A-22	<i>ay</i>
c	40	41.8	2.2	18795	9	US-10-459-352A-16	<i>ay</i>
c	41	41.8	2.2	19027	9	US-10-459-352A-13	<i>ay</i>
c	42	41.8	2.2	19181	9	US-10-459-352A-21	<i>ay</i>
c	43	41.8	2.2	19242	9	US-10-459-352A-20	<i>ay</i>

ALIGNMENTS

RESULT 1
US-10-763-179-11
; Sequence 11, Application US-10763179
; Publication No. US2004040457A1
; GENERAL INFORMATION:
; APPLICANT: HARA, SEIICHI
; APPLICANT: YOKOZU, KENZO
; APPLICANT: ABE, ISAO
; APPLICANT: TONOUCHI, NAOTO
; APPLICANT: JOJIMA, YASURO
; TITLE OF INVENTION: NOVEL PEPTIDE-FORMING ENZYME GENES
; FILE REFERENCE: 247848US0
; CURRENT FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: JP 2003-16765
; PRIORITY FILING DATE: 2003-01-24
; PRIORITY APPLICATION NUMBER: US 60/491, 612
; PRIORITY FILING DATE: 2003-08-01
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1935
; TYPE: DNA
; ORGANISM: Sphingobacterium sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (61)..(1917)
; OTHER INFORMATION:
; US-10-763-179-11
; Query Match Score 100.0%; Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAACCAAGTGTAAATTATTAATTACCCAAAGAACTACTGACAATAATTATCTGA 60
Db 1 GAAACCAAGTGTAAATTATTAATTACCCAAAGAACTACTGACAATAATTATCTGA 60
Qy 61 ATGAAAATACATACATTGCGCTTAACCTTGGCGTTTAAGGCCAGGTAACGCT 120
Db 61 ATGAAAATACATACATTGCGCTTAACCTTGGCGTTTAAGGCCAGGTAACGCT 120
Qy 121 CAAACAGTCGGCACTGGCTATGAGATCATATTGAAAGACCGAAGTGCATT 180
Db 121 CAAACAGTCGGCACTGGCTATGAGATCATATTGAAAGACCGAAGTGCATT 180

RESULT 3
US-10-855-533-11
; Sequence 11, Application US/10855533
; Publication No. US20050013864A1
; GENERAL INFORMATION:

APPLICANT: HARA, SEIICHI
 YOKOZEKI, KENZO
 APPLICANT: ABE, ISAO
 APPLICANT: TONOUCHI, NAOTO
 APPLICANT: JOJIMA, YASUO
 TITLE OF INVENTION: NOVEL PEPTIDE-FORMING ENZYME GENES
 FILE REFERENCE: 25578US0
 CURRENT APPLICATION NUMBER: US/10/855,533
 PRIOR APPLICATION NUMBER: PCT/JP03/09468
 PRIOR FILING DATE: 2003-07-25
 PRIOR APPLICATION NUMBER: JP 2002-218957
 PRIOR FILING DATE: 2002-07-26
 PRIOR APPLICATION NUMBER: JP 2003-16765
 PRIOR FILING DATE: 2003-01-24
 NUMBER OF SEQ ID NOS: 27
 SEQ ID NO: 11
 LENGTH: 1935
 ORGANISM: Sphingobacterium sp.
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (61) . (1917)
 OTHER INFORMATION:
 US-10-855-533-11

Query Match 100.0% Score 1935; DB 8; Length 1935;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1935; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAACCAAGTGTAAAATTATATAATTACACCAAAAGAATGACTGACAATAATTATCGA 60
 Db 1 GAAACCAAGTGTAAAATTATATAATTACACCAAAAGAATGACTGACAATAATTATCGA 60
 Qy 61 ATGAAAATACAAATTTCGTGCCTAAACTTTAGCGCTTTAACGGCAAGCAGTTACATGCT 120
 Db 61 ATGAAAATACAAATTTCGTGCCTAAACTTTAGCGCTTTAACGGCAAGCAGTTACATGCT 120
 Qy 121 CAAACAGCTGCCGACTCGGCTTATGTTAGCATTTAACGGCAAGCAGTTACATGCT 180
 Db 121 CAAACAGCTGCCGACTCGGCTTATGTTAGCATTTAACGGCAAGCAGTTACATGCT 180
 Qy 181 CCCATGGGAGATGGAAAATAATTATCTCGATTTACAGTCAGCTTACAGTCAGCT 240
 Db 181 CCCATGGGAGATGGAAAATAATTATCTCGATTTACAGTCAGCTTACAGTCAGCT 240
 Qy 241 AAATATCCAGTTTGCTCAATAAGAACGCCCTAACAGGTTTACCGTTACAGTCAGCT 300
 Db 241 AAATATCCAGTTTGCTCAATAAGAACGCCCTAACAGTCAGCTTACAGTCAGCT 300
 Qy 301 TATAAAAATAACTTGGAAACTTCCCAATTGTCGTTAGGCTTATTTTCGTTAAC 360
 Db 301 TATAAAAATAACTTGGAAACTTCCCAATTGTCGTTAGGCTTATTTTCGTTAAC 360
 Qy 361 CAGGATGTCCTGGCAAGTGGATGAGCAGGTTAGATGAGATACTCCGACCAAG 420
 Db 361 CAGGATGTCCTGGCAAGTGGATGAGCAGGTTAGATGAGATACTCCGACCAAG 420
 Qy 421 TACAGCAAGATAAAAAGCAATCTGATGAAAGTACCGGATACCTATGAGCTGAATGG 480
 Db 421 TACAGCAAGATAAAAAGCAATCTGATGAAAGTACCGGATACCTATGAGCTGAATGG 480
 Qy 481 TTACAGAAAATTCTCAAAAATAATAATGGCAAGCGGGCTCTANGGGATTCTPATCCA 540
 Db 481 TTACAGAAAATTCTCAAAAATAATAATGGCAAGCGGGCTCTANGGGATTCTPATCCA 540
 Qy 541 GGCTTCTTAATCTACCGTGGATTGGTCAAAACACACCCGAGCTTCCACCA 600
 Db 541 GGCTTCTTAATCTACCGTGGATTGGTCAAAACACACCCGAGCTTCCACCA 600
 Qy 601 CAGGCTCCGTAACAGACTGGTATATGGCAGACTTCCACCAATAATGGGTTATGGT 660

Db 601 CAGGCTCCGTAACAGACTGGTATATGGCAGACTTCCACCAATAATGGGTTATGGT 660
 Qy 661 CTTCAGGATGCGATTATCATGTCACATTTCATGTCACCTTTGGCTCTCCCTCCAAAACCCATTACA 720
 Db 661 CTTCTGGATGCGATTACATGTCACCTTTGGCTCTCCCTCCAAAACCCATTACA 720
 Qy 721 CGGGATCAATTAAAGGCCATAATAACTTTCGCA 780
 Db 721 CGGGATCAATTAAAGGCCATAATAACTTTCGCA 780
 Qy 781 GAAGGAGGAACAGCGGGAAACTCAAGAAAGATAATTTCGTAATCCGTACAATTGG 840
 Db 781 GAAGGAGGAACAGCGGGAAACTCAAGAAAGATAATTTCGTAATCCGTACAATTGG 840
 Qy 841 AATGACCTGTTAACATCCGACTATGATGATGATTTCGAAATCCGGTGTGATCAGAA 900
 Db 841 AATGACCTGTTAACATCCGACTATGATGATGATTTCGAAATCCGGTGTGATCAGAA 900
 Qy 901 TCTTACAGGAGGTAAACCAAGCTTGATGTTGCGTGTGCGTTTGCAGCGGAGAT 960
 Db 901 TCTTACAGGAGGTAAACCAAGCTTGATGTTGCGTGTGCGTTTGCAGCGGAGAT 960
 Qy 961 GCTTATGGAAACATTAAAGCCTACCAATCGGGATAAAAGAAAAAAACACTCG 1020
 Db 961 GCTTATGGAAACATTAAAGCCTACCAATCGGGATAAAAGAAAAAAACACTCG 1020
 Qy 1021 ATTATAGTCGGGACCTTGTATGATGGGTTGCTATGGGGTGGTTGGTGGTGG 1080
 Db 1021 ATTATAGTCGGGACCTTGTATGATGGGTTGCTATGGGGTGGTTGGTGGTGG 1080
 Qy 1081 GGTGTATCCAAATTGAGAAAACCAATTGAAACACCA 1140
 Db 1081 GGTGTATCCAAATTGAGAAAACCAATTGAAACACCA 1140
 Qy 1141 TTTCATCAAATTACCTAAAGATAAGGAAACTTGCCTTCGGAAGCTTACCTTT 1200
 Db 1141 TTTCATCAAATTACCTAAAGATAAGGAAACTTGCCTTCGGAAGCTTACCTTT 1200
 Qy 1201 GTRTCAGGCAAGGAATGGAAACATTGCAAGTGGCACCCAAAATGTAGAGACA 1260
 Db 1201 GTTTCAGGCAAGGAATGGAAACATTGCAAGTGGCACCCAAAATGTAGAGACA 1260
 Qy 1261 AAAAAACTATACCTCAACCTCAGGGAAACTTGGATTGACAAGTTCAACGTACAGAT 1320
 Db 1261 AAAAAACTATACCTCAACCTCAGGGAAACTTGGATTGACAAGTTCAACGTACAGAT 1320
 Qy 1321 CAAACGGAAACACGGGATATATGGTAGATGTCACGTTTCGCGGCTAGTCGCCCATT 1380
 Db 1321 TCCTGGATGAAATGTTACAGCCCTTAATACCTGTTCCGCACTCAGGTGGSTATT 1380
 Qy 1381 CAAACGGAAACACGGGATATATGGTAGATGTCACGTTTCGCGGCTAGTCGCCCATTCAA 1500
 Db 1381 CAAACGGAAACACGGGATATATGGTAGATGTCACGTTTCGCGGCTAGTCGCCCATTCAA 1500
 Qy 1441 GTCATGGTTTATCAAACGGAAACCGTTGACCGAGGACCTGAGATGTTGGGATATCAATGTAT 1440
 Db 1441 GTCATGGTTTATCAAACGGAAACCGTTGACCGAGGACCTGAGATGTTGGGATATCAATGTAT 1440
 Qy 1501 AACTTCTCAAAAGTTCCTCAACAGGAACAGGGACTATGTTGTCACACTGTTGAC 1560
 Db 1501 AACTTCTCAAAAGTTCCTCAACAGGAACAGGGACTATGTTGTCACACTGTTGAC 1560
 Qy 1621 GTACCTGGTGTGAGATCATGGGGAAATACCGAAAGGGCTCTANGGGATTCTPATCCA 1680
 Db 1621 GTACCTGGTGTGAGATCATGGGGAAATACCGAAAGGGCTCTANGGGATTCTPATCCA 1680
 Qy 1681 ACTCCAGGATGGTCAAAACGGTGAATTGGAAATGCCAGACGTTNGCCTACCTTCAAA 1740
 Db 1681 ACTCCAGGATGGTCAAAACGGTGAATTGGAAATGCCAGACGTTNGCCTACCTTCAAA 1740

Qy	1741	AAGGACATCCATTATGGTCTAGGTACAAACTCATGGTTCCGTCGGCAAGCAAAT	1800
Db	1741	AAGGACATCCATTATGGTCTAGGTACAAACTCATGGTTCCGTCGGCAAGCAAAT	1800
Qy	1801	CCACAGCTGTTTAGACCTTACAGCTAACACTGTTCCGCAAAACTTACCGAA	1860
Db	1801	CCACAGCTGTTTAGACCTTACAGCTAACACTGTTCCGTCGGCAAGCAAACCGAA	1860
Qy	1861	CGTATTTTCACGATGTGAACATGCCATACATCGAATTTCGCCTCAAGATTAG	1920
Db	1861	CGTATTTTCACGATGTGAACATGCCATACATCGAATTTCGCCTCAAGATTAG	1920
Qy	481	TTCAGAAAATCTCAAAACTATANTGCCAACCGGGCTCTGGATTCTTACCCA	540
Db	481	TTCAGAAAATCTCAAAACTATANTGCCAACCGGGCTCTGGATTCTTACCCA	540
Qy	541	GGCTCTATTCTACCGTCGGATGGTCAAAACACCCAGTCCTCCCA	600
Db	541	GGCTCTATTCTACCGTCGGATGGTCAAAACACCCAGTCCTCCCA	600
Qy	601	CAGCCTCCGTAACAGACTGGTATATGGGACGACTCCACATAATGGCTATTGTT	660
Db	601	CAGCCTCCGTAACAGACTGGTATATGGGACGACTCCACATAATGGCTATTGTT	660
Qy	661	CTTCAGGATGCCATTACATTCAGTCACCTTGGTGCCTCGTCACATTCATA	720
Db	661	CTTCAGGATGCCATTACATTCAGTCACCTTGGTGCCTCGTCACATTCATA	720
Qy	721	CCGATCAATTAGGCAAAATTGATCAAAAGCGATAAAATAACTTTTGCA	780
Db	721	CCGATCAATTAGGCAAAATTGATCAAAAGCGATAAAATAACTTTTGCA	780
Qy	781	GAAGCAGAACAGGGGAAACTCAAGAGAAACTTGGACTCCGTAACAATTG	840
Db	781	GAAGCAGAACAGGGGAAACTCAAGAGAAACTTGGACTCCGTAACAATTG	840
Qy	841	AATGACCTGTTAACGCACTCCGACTATGATGATTTCGAAATTCGAAAT	900
Db	841	AATGACCTGTTAACGCACTCCGACTATGATGATTTCGAAATTCGAAAT	900
Qy	901	TCTTTACAGGAGTTAACCGCTGTTGATGTTCTTGAACGGAAAGAT	960
Db	901	TCTTTACAGGAGTTAACCGCTGTTGATGTTCTTGAACGGAAAGAT	960
Qy	961	GCTTATGGACATTTAGCCTTAAACGCTTACCAATGATGAAACTTTA	1080
Db	961	GCTTATGGACATTTAGCCTTAAACGCTTACCAATGATGAAACTTTA	1080
Qy	1021	ATTTATGCGGGACCTGGTATCATGGGTTCTGGTCAAGAAGAAACTTTA	1080
Db	1021	ATTTATGCGGGACCTGGTATCATGGGTTCTGGTCAAGAAGAAACTTTA	1080
Qy	1081	GGTGATATCCAAATTGAGAAAACAGTAACTATCATGGAAACATTGAAACCA	1140
Db	1081	GGTGATATCCAAATTGAGAAAACAGTAACTATCATGGAAACATTGAAACCA	1140
Qy	1141	TTTTCAAAATTACCTAAAGATGAGAAACCTTCGCCCCCTGGAGCTAACATT	1200
Db	1141	TTTTCAAAATTACCTAAAGATGAGAAACCTTCGCCCCCTGGAGCTAACATT	1200
Qy	1201	GTTTACGGCAGGAACTCGACGATGGAAACATTCGAACTGTTGAGACA	1260
Db	1201	GTTTACGGCAGGAACTCGACGATGGAAACATTCGAACTGTTGAGACA	1260
Qy	1261	AAAAAATCTACTTCACCTCAACCTCGAGTTGAAACTTGGATGAAAGT	1320
Db	1261	AAAAAATCTACTTCACCTCAACCTCGAGTTGAAACTTGGATGAAAGT	1320
Qy	1321	TCTGGGATGAAATATGGTACGACCCATAAAACCTGTCGCAAGCTTAATT	1380
Db	1321	TCTGGGATGAAATATGGTACGACCCATAAAACCTGTCGCAAGCTTAATT	1380
Qy	1381	CAAACCAAACGGGAACTATGGTACGACCCATAAAACCTGTCGCAAGCTTA	1440
Db	1381	CAAACCAAACGGGAACTATGGTACGACCCATAAAACCTGTCGCAAGCTTA	1440

1021 ATTTAGTCGGGACCTGGTATCATGGGGTTCGGCAAGGGAAACTATTAA 1080
 Db 1081 GTGTGATTCAAATTGAAAAAACCGTATTACTTACGGAAACATTGAAACACA 1140
 Qy 1081 GTGTGATTCAAATTGAAAAAACCGTATTACTTACGGAAACATTGAAACACA 1140
 Db 1081 GTGTGATTCAAATTGAAAAAACCGTATTACTTACGGAAACATTGAAACACA 1140
 Qy 1141 TTTTCATATAATTACCTAAGATGAAACTTCGCCCTTCGAAGTAACTTT 1200
 Db 1141 TTTTCATATAATTACCTAAGATGAAACTTCGCCCTTCGAAGTAACTTT 1200
 Qy 1201 GTTTCAGCAGCAACGAAACTTCAAGAACAGTGCCACCAAAATGTAGAGCA 1260
 Db 1201 GTTTCAGCAGCAACGAAACTTCAAGAACAGTGCCACCAAAATGTAGAGCA 1260
 Qy 1261 AAAAACTATACTTCACACTCGGGAAACTTGGATTGAGAAAGTCAACGTACAGAT 1320
 Db 1261 AAAAACTATACTTCACCTAGGGAAACTTGGATTGAGAAAGTCAACGTACAGAT 1320
 Qy 1321 TCTCGGGATGAAATTGTPAACAGCCPTAATAAACCTTCCCACATCAAGTGGCTTAATT 1380
 Db 1321 TCTCGGGATGAAATTGTPAACAGCCPTAATAAACCTTCCCACATCAAGTGGCTTAATT 1380
 Qy 1381 CAAACCCAAACACGGAACTTATGGTAGATGATCAACGTTTGGCCCTGTAT 1440
 Db 1381 CAAACCCAAACACGGAACTTATGGTAGATGATCAACGTTTGGCCCTGTAT 1440
 Qy 1441 GTCATGGTTTATCAAACGAAACGTTGAGGGACCTGACATAGTAGGCCAACTCAA 1500
 Db 1441 GTCATGGTTTATCAAACGAAACGTTGAGGGACCTGACATAGTAGGCCAACTCAA 1500
 Qy 1501 AACTTTCMCAAACTTCTCAACAGGAAACGAGGCAACTATGTTGCAAACTGATTGAC 1560
 Db 1501 AACTTTCMCAAACTTCTCAACAGGAAACGAGGCAACTATGTTGCAAACTGATTGAC 1560
 Qy 1561 GTTTATCGGAATGCGCAAGTTATGCTGAAATTCAGGAAACTATGTTGCAAACTGATTGAC 1620
 Db 1561 GTTTATCGGAATGCGCAAGTTATGCTGAAATTCAGGAAACTATGTTGCAAACTGATTGAC 1620
 Qy 1621 GTCAGTGGTGGATGATCATGGGGAAATACCGAAATGGTTGGATAAAGGCCAGGGCTTG 1680
 Db 1621 GTCAGTGGTGGATGATCATGGGGAAATACCGAAATGGTTGGATAAAGGCCAGGGCTTG 1680
 Qy 1681 ACTCCAGGTATGGTCAAGTGAAGGTGAATTGGTAATGGCAAGCGTGGCATACCTTCAAA 1740
 Db 1681 ACTCCAGGTATGGTCAAGTGAAGGTGAATTGGTAATGGCAAGCGTGGCATACCTTCAAA 1740
 Qy 1741 AAAGGACATTCGCAATTATGGTCAGGTACAAAACCTCATGGTTCGGTGGCAAGAAAT 1800
 Db 1741 AAAGGACATTCGCAATTATGGTCAGGTACAAAACCTCATGGTTCGGTGGCAAGAAAT 1800
 Qy 1801 CCACAGGGTTTTAGCAACCTTATACAGCTACCAAAAGCTACCCAA 1860
 Db 1801 CCACAGGGTTTTAGCAACCTTATACAGCTACCAAAAGCTACCCAA 1860
 Qy 1861 CGPATTTTCACCATGAAACATGCCACATCATGAAATTCTGCTCAAGATTAG 1920
 Db 1861 CGPATTTTCACCATGAAACATGCCACATCATGAAATTCTGCTCAAGATTAG 1920
 Qy 1921 CAGGTAATTGCGAA 1935
 Db 1921 CAGGTAATTGCGAA 1935
 Qy 541 GGCTCTPATCPACCGGTTGATGGCTTGGTCAACACCCGAGCTCTCCCA 600
 Db 541 GGCTCTPATCPACCGGTTGATGGCTTGGTCAACACCCGAGCTCTCCCA 600
 Qy 601 CAGGCCTCCGTAACAGACTGTTGATGGCTTGGTCAACACCCGAGCTCTCCCA 660
 Db 601 CAGGCCTCCGTAACAGACTGTTGATGGCTTGGTCAACACCCGAGCTCTCCCA 660
 Qy 661 CTTCAAGATGCAATTACATTGCAACCTTGTGTTGATGGCTTGGTCAACACCCGAGCTCTCCCA 720
 Db 661 CTTCAAGATGCAATTACATTGCAACCTTGTGTTGATGGCTTGGTCAACACCCGAGCTCTCCCA 720
 Qy 721 CGGGATCAATTAGGGCAAAATTCAAGATCAAAGAACCGATAAAATAATACCTTTGCA 780

RESULT 6

US-11-050-829-19

Sequence 19, Application US/11050829

Publication No. US200501761501

GENERAL INFORMATION

APPLICANT: KIRI, IKUO

YOKOZEKI, KENZO

SUZUKI, SONOKO

MIHARA, YASUHIRO

APPLICANT: HIRAO, YOSHINORI

721 CCGGATCATTAAAGCCAAATTACATCAAAGGCCGATAAATACTTTTGC 780
 781 GAGGAGGAAGCGGGAACTCAAGAAAGAAGTATTGTTGTACTCGTACAATTGG 840
 781 GAGGAGGAAGCGGGAACTCAAGAAAGAAGTATTGTTGTACTCGTACAATTGG 840
 961 ATGACCTGTTAACATCCGACTATGATGATTGTTGAAATTCGCGTGTATCAGAA 900
 841 ATGACCTGTTAACATCCGACTATGATGATTGTTGAAATTCGCGTGTATCAGAA 900
 901 TCTTATAGGAGTAACACCACTGATGTTGTTCTTGAGCGGAAAGAT 960
 901 TCTTATAGGAGTAACACCACTGATGTTGTTCTTGAGCGGAAAGAT 960
 961 GCTTATGAACTATTAGACCTAACATGATTGAGGATAAAGGAAAACACTG 1020
 961 GCTTATGAACTATTAGACCTAACATGATTGAGGATAAAGGAAAACACTG 1020
 1021 ATTTTACTGCGGGACCTTGGATCATGGCTTCTGCGAAGGAAACTPATTAA 1080
 1021 ATTTTACTGCGGGACCTTGGATCATGGCTTCTGCGAAGGAAACTPATTAA 1080
 1081 GGTGATATCAGTTAGACCTAACATGATTGAGGATAAAGGAAAACACTG 1140
 1081 GGTGATATCAGTTAGACCTAACATGATTGAGGATAAAGGAAAACACTG 1140
 1141 TTTTCAAAATTACCTAAAGATGAGGAAACTTGGCCCTTCGAGCTAACATTTT 1200
 1141 TTTTCAAAATTACCTAAAGATGAGGAAACTTGGCCCTTCGAGCTAACATTTT 1200
 1201 GTTTTCAAAATTACCTAAAGATGAGGAAACTTGGCCCTTCGAGCTAACATTTT 1260
 1201 GTTTTCAAAATTACCTAAAGATGAGGAAACTTGGCCCTTCGAGCTAACATTTT 1260
 1261 AAAAAACTTACTTCCAACTCAGGGAAACATTGGCAACAGTGGGAAACTTGG 1320
 1261 AAAAAACTTACTTCCAACTCAGGGAAACATTGGCAACAGTGGGAAACTTGG 1320
 1321 TCCTGGGATGATGATATGTAACAGACCCATAAACCTGGCATCAAGTGGGTAATT 1380
 1321 TCCTGGGATGATGATATGTAACAGACCCATAAACCTGGCATCAAGTGGGTAATT 1380
 1381 CAAAACCGAACACGGGATGATATGGTAGATGTAACGTTGCGCCTGTAT 1440
 1381 CAAAACCGAACACGGGATGATATGGTAGATGTAACGTTGCGCCTGTAT 1440
 1441 GTATGGTTTATCAACGGAACGGTATGGTAGATGTAACGTTGCGCCTGTAT 1500
 1441 GTATGGTTTATCAACGGAACGGTATGGTAGATGTAACGTTGCGCCTGTAT 1500
 1501 AACTTTCTCAAGTTCTCAAGGAAACAGGAACTGTTCAACTGTTGAC 1560
 1501 AACTTTCTCAAGTTCTCAAGGAAACAGGAACTGTTCAACTGTTGAC 1560
 1561 GTTATCGAAATGATGCGAGCAAGTTCAAGGAAACATGGCTGATTCAAATGATG 1620
 1561 GTTATCGAAATGATGCGAGCAAGTTCAAGGAAACATGGCTGATTCAAATGATG 1620
 1621 GTACGTTGAGATGTTGAGATCATGGCGGAAATACCGAAATGGTTGATAAAGG 1680
 1621 GTACGTTGAGATCATGGCGGAAATACCGAAATGGTTGATAAAGG 1680
 1681 ACTCCAGTATGCTGAAAGTGAATTGTAACGTTGCAACTTCAA 1740
 1681 ACTCCAGTATGCTGAAAGTGAATTGTAACGTTGCAACTTCAA 1740
 1740 CGAAAGATAAAAAGGAAATCATGAAAGTAGGATGCTGAAATGGTTAC 1740
 1740 CGAAAGATAAAAAGGAAATCATGAAAGTAGGATGCTGAAATGGTTAC 1740
 1741 AAAGGACATCGCATTATGGTTGAGTACAACACTATGGTTCCGCTGAAACAA 1800
 1741 AAAGGACATCGCATTATGGTTGAGTACAACACTATGGTTCCGCTGAAACAA 1800
 1801 CCACAGGTGTTAGACCTATAAGCTACAGTACCCATAAGCTACCCAA 1860

Result 7
 US-10-763-179-5
 Sequence 5 Application US/10763179
 Publication No. US20040204577A1
 GENERAL INFORMATION:
 ; APPLICANT: HARA, SEIICHI
 ; APPLICANT: YOKOZEKI, KENZO
 ; APPLICANT: ABE, ISAO
 ; APPLICANT: TONOUCHI, NACHTO
 ; APPLICANT: JOJIMA, YASUO
 ; TITLE OF INVENTION: NOVEL PEPTIDE-FORMING ENZYME GENES
 ; FILE REFERENCE: 247848US0
 ; CURRENT APPLICATION NUMBER: US/10/763,179
 ; CURRENT FILING DATE: 2004-01-26
 ; PRIORITY APPLICATION NUMBER: JP 2003-16765
 ; PRIORITY FILING DATE: 2003-01-24
 ; PRIORITY APPLICATION NUMBER: US 60/491,612
 ; PRIORITY FILING DATE: 2003-08-01
 ; NUMBER OF SEQ ID NOS: 27
 ; SEQ ID NO 5
 ; LENGTH: 204
 ; TYPE: DNA
 ; ORGANISM: Empedobacter brevis
 ; FEATURE: CDS
 ; NAME/KEY: CDS
 ; LOCATION: (61) . (1908)
 ; OTHER INFORMATION:
 US-10-763-179-5

Query Match 39.3% ; Score 771; DB 8; Length 204;
 Best Local Similarity 65.1%; Pred. No. 7.8e-201;
 Matches 1144; Conservative 0; Mismatches 600; Indels 3; Gaps 1;
 125 CAGCTCCGACTCGGGTTATGGAGATCATTATGAAAGAACGGAATTCCCA 184
 134 CAAAGAGATGGAAAAMAAATTATTCAGTGGATCTACGTTGCAATTTCGA 193
 185 TGCGAGATGGAAAAMAAATTATTCAGTGGATCTACGTTGCAATTTCGA 184
 194 TGCGCAGATGGACAAGTTTACGCTATTATAGCCTAAAGTAAACAAACAAAT 253
 245 ATCCAGTTGCTCATTAGGCGCTTACAGGTTTACCTTATGGCGAGCGATA 304
 254 ATCCCGTTTGTAAATCGTACGGCTTATACAGTTCGCTTATGGTGTAAATGAAATCA 313
 305 AAAAAGCTTGGAAACTTTCCCAAATGATGCGTGAAGGTATATTTCGTTACAGG 364
 314 AGAAATGTTGAGAATTTCCTAGGAAATGGTTTATGGTTTGTGAG 373
 365 ATGTCCTGCGGAAAGTGATGCGGAAGGTGATTTCAGGATATACTGGATTTCGCTG 493
 434 CAARAGTAAAGGAAATGCAAGTACATGATAGCTGAGATTCACCTTAAATCTT 554
 485 AGAAAATCTCAAACACTATGGCAAAAGCTGATGCGTGAATGGTTAC 553
 494 CTAAAACCTTACGCTTACAGCTACCCATAAGCTACCCAA 553

Db	254 ATCCGTTTGTAAATGCTACGCCATTACAGTCGGTCTATGGCTAATGATAACA	313	Db	1331 TTGACGAATAATGTTGCAGATCCAAATTCTCCAGTCCTTATTCAAGGAGGTTTAGAAA	1390
Qy	305 AAAAACCTGGAAACTTCCCRAATGATGGTGAAGGTTACCGG	364	Qy	1385 ACGAAACGGGAGTATGGTAGATCACTGAGCTTGCCTGATGCCCTGATGTC	144
Db	314 AGAAATCGTTAGAAATTCTCACGAAATGGCAGGTTATTTTACCGAG	373	Db	1391 CTGGTTAGAGATAATGGTCGATGATCAGCTTGCTTACTGCTGTGTT	1450
Qy	365 ATGTCGGCACTGGTGAAGTGGTGAAGATAACGTCGACCGTACA	424	Qy	1445 TGTTTATCAAGGAAACCCGTTGACGGAGCTGAGATACTGGCCAACTCAA	1504
Db	374 ATGTGAGGAATGGGAAATGGTGAAGATGGTGAAGCTATAATCCTT	433	Db	1451 TGTGTTCAATCTGATATTGACAGATAATGCTGTATCATAC	1510
Qy	425 GCAAGATAAAAGCAATCGTAAGCTGATGGCTTGTGTTAC	484	Qy	1505 TTCTAAAGTTCTCAACAGAACAGACGGGAGTATGGTCAACTGAGCTT	1564
Db	434 CAAAAGTAAAGGCAATTGCGAAACACAGATACTTGTAGATGGCTTG	493	Db	1511 ATTAGTGGTTCTACTACGGGAAACAGCTGATGTTAAATTGATGTT	1570
Qy	485 AGAAAATCTCAAAACTATAATGGCAAGAACGGCTTATCCAGCT	544	Qy	1565 ATCGGATGATGCGAAGTATCAAGGTTGATACTAAATGCTGATGTC	1624
Db	494 CTAAARCTTGTGAAATTACGAAAGLACTGCGTAATTGCTCTGTT	553	Db	1571 ATCTGAAAACGCCAAATTATAACAAATTGCTGATATCAAATTGATT	1630
Qy	545 TCTATTCTACCGTGGATTGGTCAAACACCCGAGCTGGCCAGGG	604	Qy	1625 GTGGTGGATCATGGCGGGAAATACCGAAATGGCTGACTC	1684
Db	554 TTATTCCACAATGAGTGGTAAATGCTAACTTAAAGGGTTGCGCAG	613	Db	1631 GTGCGAAATTGCGGAAATATGCGGAAATATGTTCTAACCGGAAGT	1690
Qy	605 CTCCCGTAAACAGCTGTTATCGGCCAGCACTTCCACATAATGGCTATGTTCTC	664	Qy	1685 CAGGTATGGTCAAAGGTGAATTGAAATGCCAGCTGCGCATACCTTCAAAAG	1744
Db	614 CGCCCGTAAACCAATTGGTTTGTGCGATTTCATCATATAATGGGTTTATTCUTGA	673	Db	1691 CGAAATTAAAGAAACAAATGTAACGTAACGATECCGAGTGGACATTAAGAAAG	1750
Qy	665 AGGATGTTAACATTGCTGTCACCTTGTGTCAAAACCATTACCCGG	724	Qy	1745 GACATCCCATATGGTTCAGGTACAAACTCATGGTTCCGTTGCGAAGAACATCC	1804
Db	674 ATGATTCTTCTCATTTGACTTGTGACTTTTGGTGTAAACGTCGCAACATTACGCCAG	733	Db	1751 GACATCCCATATGGTTCAGGTCAAGTCAAGTGGTTCCCTTGGAGATGCCAATCGC	1810
Qy	725 ATGATTAAAGGCCAAAATTCAAGTAAATTAATRACTTTTGCGAGAG	784	Qy	1805 AGGTGTTTACCACTTATACGCTTACCAAAAGCTGATTTCCGAAAGCTTACCAAGTA	1864
Db	734 ATAAAGCTCGAAAACGTTGAAATGTTAGTATGTTATGCT---AA	790	Db	1811 AACAAATTAAAGTGTGTTACGAAAGCAACTTCTAAAGATAATTAAACAAACGAA	1870
Qy	785 CAGGAACGGCGGAAACTCAAGAAAGTATTGTTGACTTCGTAACATTGGAAAG	844	Qy	1865 TTTCAC 1871	
Db	791 GTGGCTCTGTAAGAGTGTGAAAGATAATTGCAAGATAATGTTACATG	850	Db	1871 TTATCA 1877	
Qy	845 ACCGTGTTAGCATCCCACTATGATGTTTGGAAATCGGTGTATCAGAACTT	904	RESULT 10		
Db	851 ATTATTTCGCTTCAGATTAGCTGATTTGGCAAGTGTATGTTACCACTT	910	US-10-859-405-5		
Qy	905 TACAGGAGGTAAAACCACTGCTGATGTTGGTGTGTTCTTGAGCGGAAGATGCTT	964	; Sequence 5, Application US/10859405		
Db	911 TAATCAAGTGTGCAACCTCTGTTGAGTGGTGTGTTTTGTGAGAGATGCT	970	; Publication No. US200500321541		
Qy	965 ATGGAACCTTTAGACCTTACCATGATGTTGGAAATGGCAAACACTGATT	1024	; GENERAL INFORMATION:		
Db	971 ACGGCGTTTCGAAACGTATAAGCAAACTCGAAAGCAAAATTATA	1030	; APPLICANT: YOKOZEKI, KENZO		
Qy	1025 TAGTCGGGGACTTGTGATGTTGGCTTCTGGCAAGGAAACTTGTG	1084	; APPLICANT: SUZUKI, SONOKO		
Db	1031 TGGTGGCGGACTTGTGTTCTGGTGTGTTCTAGGAGACTTGTGAG	1090	; APPLICANT: HARA, SEIICHI		
Qy	1085 ATATCCAAATTGAGAAACCACTTACATCTACGGAAACATTGAAACCAATT	1144	; APPLICANT: ABE, ISAO		
Db	1091 ATATGAACTTGTGATGTTGGCTTCTGGTGTGTTCTGGTGTGAG	1150	; TITLE OF INVENTION: METHOD FOR PRODUCING TRIPPIPEPTIDES AND/OR PEPTIDES LONGER THAN		
Qy	1145 TCAATATTACCTAAAGTGAAGGAAACTTGTGATGTTGGCTT	1204	; FILE REFERENCE: 254070US0		
Db	1151 TAAATTATTACCTAAAGTAAAGTAAACCTTAAACCACTTGTGAAAC	1210	; CURRENT APPLICATION NUMBER: US/10/859,405		
Qy	1205 CAGGAGCAACCTAACCTAACGTTGCAAGTGTGAGCAAA	1264	; CURRENT FILING DATE: 2004-06-03		
Db	1211 CGGGATCTAACGAAACATTGTGTTGGCAACAAATGTCACAA	1270	; PRIOR APPLICATION NUMBER: US 60/491,547		
Qy	1265 AACTATACCTAACCTAACGTTGCAAGTGTGAGCAAACTTGTGCT	1324	; PRIOR FILING DATE: 2003-08-01		
Db	1271 AAATTATTGCAACAAATGCTTTAAATAAACCAATACAAACTCTT	1330	; PRIOR PILING DATE: 2002-07-26		
Qy	1325 GGATGATAATGTAACGACCTTAATAACCTGTTGCGATCAAGTGGGTAATC	1384	; NUMBER OF SEQ ID NOS: 21		
			; SEQ ID NO 5		
			; LENGTH: 2024		
			; TYPE: DNA		
			; ORGANISM: Empedobacter brevis		
			; FEATURE: CDS		
			; NAME/KEY: CDS		
			; LOCATION: (61) .. (1908)		
			US-10-859-405-5		
			Query Match 39 8%; Score 771; DB 8; Length 2024;		
			Best Local Similarity 65.5%; Pred. No. 7.8e-201;		
			Matches 1144; Conservative 0; Mismatches 600; Indels 3; Gaps 1;		
			125 CAGCTCGGACTCGGCTTGTGTTAGATCATTGAAAGCCGAAGTAGCCAAATGCC		
			Qy		

Db	134	CATAAGCAGATTCTGCTATGTCGCAATTAGAACAACTTACGAAAATAGAACAACTTACGGA 193	Db	1211	CGGGATCTAACATTGAAACCATTTGATGCTTGGCACCCAAAATGTACAAACACAA 1.270
Qy	185	TGGAGATGGAAAAAATTATTAACTGGATCTAACGTCACAGCTCCAAAGAACAAATCAGAAAT 244	Qy	1265	AACTATACCTTCAAACCTCAGGGAAACTTGATTGACAAGTCAACGTACAGATTCCT 1324
Db	194	TGCGCGATGGTACAAAGTTAACGTTTAACTACGGTAAATTAACGAAAGATAAAACAAAT 253	Db	1271	AAATTATTGCAACAAATGCTAAATTAACAAACAACTACTT 1330
Qy	245	ATCCAGTTTGCCTAATGAAACCCCTAACCGTTTCCCTATGGCAAGACGAACTTA 304	Qy	1325	GGGATGATATGTAACAGACCTATAAACCTGTCGGCATCAAGTGGGTAAATCATAA 1384
Db	254	ATCCGTTTGTAAATGTAATGCTGCCCTTACAGTTTGTGTTAATGATRCA 313	Db	1331	TTGNCBAGATATTGCGATCCAACTTCTCAGTTTGTGAGTTTGTGAGAA 1390
Qy	305	AAAAAGCTGGAAACTTCCCCTAAATGATCGTGAAAGCTTATTTCTGTTACAGG 364	Qy	1385	ACCGAGACGGAGTATATGGTAGATCAACGTTGCGCCTGAGCTGAGCTCA 1444
Db	314	AGAAATCCTTAGEAAATTCTTACAGAAATGGCTTACAGGTTTGTGTTACCAAG 373	Db	1391	CTCGTTAGAGAAATATGGCTGATCAACGTTGCTACTGTCCTGATGTTA 1450
Qy	365	ATGTCCTGGCAAGTGTGAGATAATACGTCGACCGTCA 424	Qy	1445	TGGTTTATCAACGGACCCGTGACCGAGCTGAGCTGAGATGTTGGCCCATCANAAT 1504
Db	374	ATGTGAGGAAATGGTGGAGCTTCACTAAATCCTT 433	Db	1451	TGGTGTATCACTGATATTGCAAGAATATTAGCTGCTGCTGTTATGATC 1510
Qy	425	GCAAGATAAAAGCANTGATGAAAGTACGGATACTTATGTCGCTGAAATGTTAC 484	Qy	1505	TTCTCAAGGTTCTCAACAGAAACAGACGGCACTATGTTGCAACATGTTGAGCTT 1564
Db	434	CTAAAAGTAAAGGCAATTGCGAACACAGATACTTGTACCTAGATGATGCTGT 493	Db	1511	ATTTAGTGGTTCTAATACGSEARAGACGTGATTTGTGTAATTGTTGATTTT 1570
Qy	485	AGAAAATCTCAAACATAATGCAAAGCGGGCTCTATGGATTCCPATCCAGCT 544	Qy	1565	ATCCGATGATGATGCAAGTATCAAGAAAACAAATGGTGTATCAATGTTGAC 1624
Db	494	CTAAAACCTGAGAAATTACGAAAAGCTTACAGAAATGGCTGAAATTCTGTT 553	Db	1571	ATCCGTAAAACGCCAAATTAAACACATTATGGTGTATCAAAATTGATTCATTGTC 1630
Qy	545	TCPATTCTACCCTGGATGGTCAAACACACCCGGCTTCCCGCAGGG 604	Qy	1625	GTGGTGTGAGATCATGCCGGAAATACCGAAATGGTTTGTGATAAGGGAGCTGACT 1684
Db	554	TTCATTGCAACATGGATTGGTTAAATGCGATCCAACTCTAAAGCGGTTGCGCACAG 613	Db	1631	GTGCGAAATTATGGCGGAAATATTAGAAATAGTTCTAACCCTGGAAGCTATGTT 1690
Qy	605	CNCCCGTAACAGACTGGTATAATGGCAGCTTCCACACATAATGGGTTCTC 664	Qy	1685	CAGGTATGGTCAAAGGTGATTGAAATGCAACGTTGCGTACAGTGGCAATGTT 1744
Db	614	CGCCCGTACCAATTGGTTAGGTGAGCTTTCATCATATGGAGTTTATCTGA 673	Db	1691	CGAAATGAAAGAACAAATGTAACGTTGCAAGTGGCAATACATTAAAG 1750
Qy	665	AGGATGGATTACATTCTGTCACCTTGGTGTCCCTGTCAAAACCATTACCG 724	Qy	1745	GACATGCCATTATGGTTCAACTGTTCCCTGGGAAAGGAATCCAC 1804
Db	674	ATGATTCTCTCATTTGACTTTGGTGAATTCATAAAGTATTATGTTATGCA - -AA 790	Db	1751	GACATGCCATTATGATTCAAGTCAAGTGGTGTCTTAAAGTGTGCAATCGGC 1810
Qy	725	ATCAATTAAAGGCAAATTCTGAGTAAAGAGCCATAATAACTTTTGCGAG 784	Qy	1805	AGGTGTTTGTAGCACCTTACAGCTTACAGTAAAGCTGATTTCCGCAAGCTAACGTA 1864
Db	734	ATAAAGGTCGCAAACGTTGGTGAATTCATAAAGTAAATGTTTGTGAAAC 733	Db	1811	AAACAATTATGATTTGTTACGAAAGCAACTCTTAAAGTATTAAACAAACGCAACGAA 1870
Qy	785	CAGGAACAGCGCGGAACCTCAAGAAGAATTTGGTACCTGAACTTGGAG 844	Qy	1865	TTTTCA 1871
Db	791	CTGGCTCTGTAAGGTGAGATAATAATTGCAAGTATTCAGTTTACATG 850	Db	1871	TTTATCA 1877
Qy	845	ACCTGTTAACGATCCTGGACTATGATGATTTGGAAATTCGGTGTGATCAAGTCTT 904	RESULT 11 US-10-876-673-5		
Db	851	ATTATTGCGCATCCAGATTAACGATTAATTGGCAAGATGTTTACACATT 910	; Sequence 5, Application US/10876673		
Qy	905	TACAGGGGTAAACCGCTGATGTTGGTGTCTTGTGCGGAAAGATCTT 964	; Publication No. US2005124354A1		
Db	911	TAACTAAGCTGCAACCTGCTGAATGAGCTGTTTGTGAGAAGATGTT 970	; GENERAL INFORMATION:		
Qy	965	ATGAAACATTAGACCTACCAATGATGTTGAGATAAAAGCRAAAACACTCAT 1024	; APPLICANT: YOKOZEKI, KENZO		
Db	971	ACGGCGCTTTCGAAACCTTACGAAATTGAAACAAACTTACGAACTT 1144	; APPLICANT: OHNO, AYAKO		
Qy	1025	TAGTCGGGACCTTGTGATCATGGCGTGGTTCTGGCAAGGAAACTATTAGGTG 1084	; APPLICANT: HARA, SEIICHI		
Db	1031	TGTTGCGGACCTTGTGTTCTGGTGTGAGTACTTTGGAG 1090	; APPLICANT: ABE, ISAO		
Qy	1085	ATATCCAAATTGAGAAAACGACTTACGTTGAACTTACGAACTT 1150	; TITLE OF INVENTION: METHOD FOR PRODUCING ALPHA-L-ASPARTYL-L-PHENYLALANINE-BETA-ESTER		
Db	1091	ATATGCAATTGCTGCAATGAGTAAATGAAATTGCGCTT 1150	; TITLE OF INVENTION: AND METHOD FOR PRODUCING ALPHA-L-ASPARTYL-L-PHENYLALANINE-ALPHA-METHYL ESTER		
Qy	1145	TCAAATATACCTAAAGTGGGAACTTACGTTGAGTAACTT 1204	; TITLE OF INVENTION: ALPHA-L-ASPARTYL-L-PHENYLALANINE-ALPHA-METHYL ESTER		
Db	1151	TTAATTATTACCTAAAGTAAAGCTTAAACCAACCGAAGTACATT 1210	; FILE REFERENCE: 254816US0PCT		
Qy	1205	CAGGCAACGAACTTCCGACCTTACGTTGAGTACGGAACTT 1264	; CURRENT APPLICATION NUMBER: US/10/876, 673		
		; CURRENT FILING DATE: 2004-06-28			
		; PRIOR APPLICATION NUMBER: PCT/JP2004/000620			
		; PRIOR FILING DATE: 2004-01-23			
		; PRIOR APPLICATION NUMBER: JP 2003-016764			
		; PRIOR FILING DATE: 2003-01-24			
		; PRIOR APPLICATION NUMBER: JP 2003-201819			
		; PRIOR FILING DATE: 2003-07-25			
		; PRIOR APPLICATION NUMBER: US 60/491, 546			
		; DPAIR FILING DATE: 2003-08-01			
		; NUMBER OF SEQ ID NOS: 27			
		; SOFTWARE: Patentin version 3.3			
		; SEQ ID NO 5			

; LENGTH: 2024
; TYPE: DNA
; ORGANISM: Empedobacter brevis
; NAME/KEY: CDS
; LOCATION: (61)..(1908)
; US-10-876-673-5

Query Match	39.8%	Score 771; DB 9; Length 2024;	
Best Local Similarity	65.5%; Conservative Matches 1144;	Pred. No. 7.8e-201; Mismatches 600; Indels 3; Gaps 1;	
Qy	125	CAGCTGGGACTGGCTATGGTAGATCAATTGAAAGACCGAGTAGCAATTCCA 184	
Db	134	CAAAGRGATCTGGCTATGGCGRNCAATTAGAAAGTAACTTCGA 193	
Qy	185	TGGAGATGGAAAAAATTAACTGGATCTACACTCCAAAAGACAATTCCAAGAAAT 244	
Db	194	TGGCGATGGTAGAAGTTAACGGTAAATTACAGCAAAAGATAAACACAT 253	
Qy	245	ATCCAGTTTGTCTCATAGAACGCCCTAACCGTTAACCTTATGGCAGAGATA 304	
Db	254	ATCCCGTTTGTAAATGTAACAGTTGCCCTPATACAGTTGCCCTATGGCTAAATGATA 313	
Qy	305	AAGAAAGCTTGGAAACTTCCCACAAATGGTAAAGCTTACCGG 364	
Db	314	AAGAACTTGGAAATTCTTCAAGAACCTTACAGAAATGGCAGGGTTTACCAAG 373	
Qy	365	ATSTCCCTGGCAAAGTGGATGAGCTGATTGAAAGATAACCTCGACCACSTACA 424	
Db	374	ATGTGAGGGAAATGGTAGGGAAACGGGAATTTGGATTTGAACTATAATCCTT 433	
Qy	425	GCAAGATAAAAGCATTCTGATGAACTACGGATACTTACATGCCCTGATGGTAC 484	
Db	434	CAAAAGTAAAGGCAATTGCAAAACGACAGATACTTGTAACTCTAGATGGCTTG 493	
Qy	485	AGAAAATCTAAAACTATAATGGCAAAAGCGGGCTCATGGATTCCPATCCAGCT 544	
Db	494	CTDAAACTTGGAGAAATTACAGATGGTAAATTGGCATCAAACGGCTGAATTTCGATCTCTGTT 553	
Qy	545	TCTATTCTACCCCTGGATTGGTCAAAACACACCCGAGCTGGCATGTCCTCCACAGG 604	
Db	554	TTTATTCGACAATGAGTTGGTAAATTGGCATCAAACCTCAAACGGCTGAATTTCGCAAG 613	
Qy	605	CTCCCGTAACAGCTGGTATATGGCGAACGTTCCACCATATGGGTATGGTTCTC 664	
Db	614	CGCCCGTAAACCAATTGGTTTGGATTTCATCATATACTGGATTTTATTCTGA 673	
Qy	665	AGGATGCTTACATTCTGTCACCTTGGTCTCCCTGTCACACCCATTACACGG 724	
Db	674	ATGTTCTCTCATTTGACTTTTGGTAAACGTCGCACCAATTACGCAG 733	
Qy	725	ATCAATTAAAGGCAAAATTAGATCAAAGAAGCCATAATAACTTTTGGCAGAG 784	
Db	734	ATAAGGTCGAAACGTTGGATATCCGATAAAAGATAATTAGATTTATGTC---AA 790	
Qy	785	CAGGAACGGCGGAAACTCAAGAACAGTATTGGTAGCTCCGTAACATTGGATG 844	
Db	791	GTGGCTCTGTAAGAGTAAATTTGCAAGATAATTCAGTTTACATG 850	
Qy	845	ACCTGTTAAGCATCCGACTATGATGTTTGGAAATCGCGTGTCAAGTA 904	
Db	851	ATTATTGGCATCCAGATTACGATATTGGCAGATCTAATGTTTACACATT 910	
Qy	905	TACAGGAGTAAACCAAGCTGTGATGCTGGTCTGGTCTGGCTGAGATCTA 964	
Db	911	TAACTAACGGCACCTGTGATGACCGTTGGTGGAGATCT 970	
Qy	965	ATGGAACCTTAAACCTAACCTGATGAGATAAAGCAAAACACTCCATT 1024	
Db	971	ACGGCGCTTTCGAAACGTTAAAGCAAAATCGAAAGCAAAATPA 1030	
Qy	1025	TAGCTGGGACCTTGTATCATGGGGTGGTTCTGGCAGAGGAACATTAGGTG 1084	

Db 1031 TGGTGTGGGACCTTGTATGGGGTGGTTCTGGCAGAGGAACATTAGGTG 1090

Qy 1085 ATATCCATTGAGAAAACGATGAACTTATGAGAACTTGGCAACCATTT 1144

Db 1091 ATATGGATTGCGATGAACTTGGCAACCATTTGGCTT 1150

Qy 1145 TCAAATTACCTAAAGATGGAAAACCTGCCCCCTGGCAAGCTAACATTGTT 1204

Db 1151 TAATTAATTACTAAAGATAAGTAAAGTAAACCAACGAGTCAATTGTT 1210

Qy 1205 CAGGAGGAAAGAAACATTGAAACAGTGGCACC AAAAATGTAGAGCAAAA 1264

Db 1211 CGGATCTAACGAATGAAACATTGATGCTGGCACC AAAAATGTAACACACAA 1270

Qy 1265 AACATACCTAACCCCTAGGGAAACCTGAACTGAACTTACAAAGTTAACGTA 1324

Db 1271 AAATTATTGCAACAAATGTTAAATACACCAATACACAACACTTT 1330

Qy 1325 GGGATGATAATGATCTAACGACCCATAAACCTGTCGGCATCAAGGTGGGTAATTCAAA 1384

Db 1331 TTGAGGAAATGTTGAGATCCAAATCTCAGTCAAGGGAGTTTGTGAA 1390

Qy 1385 ACCGAAACACGGGAGTATATGGTAGATCAACGTTTCGCGCTGACTCGCTG 1444

Db 1391 CTCTGTCAGAGAAATATGCTGATCAACGCTTCTGCTCTGATGTT 1450

Qy 1445 TGGTATTAACAGGACCGTGAAGCTGAGATGAGTGAACGGAGGACTCTG 1504

Db 1451 TGGTGTATCACTGATATTGCAAGAATATTAGCTTGTGCTGTTCTGTT 1510

Qy 1505 TTCTCAAAGTTCTCAACGAAACAGACGGCAATATGTTGACCTTT 1564

Db 1511 ATTAGTGGTTCATGAGGAAACAGCTGAACTTACAGCTGAAATTTGTTGATGTT 1570

Qy 1565 ATCCGATGATGAGCAAGTTATGCAAGGAAAACAACTGCAATGTTGTCAC 1624

Db 1571 ATCCGTAACACGCCAAATTATAACALATTATGCTGATATCAAAATTGATTC 1630

Qy 1625 GTGGTAGATCATGGGGAAATACCGAATGGTTGATAAGGCGAGCTGACTC 1684

Db 1631 GTGCGTAACATTGGCGGAAATAATGAGATACTTCTCAACCCGAAAGTATGTT 1690

Qy 1685 CAGGTATGGTCGAAACGTTGAAATGCTGCAATCCCTCAAAAG 1744

Db 1691 CGAAATAGAAACAAATGTAACGTAACGATGTCAGTAACTTAAAGAAG 1750

Qy 1745 GACATCCCATATGGTTCAAGTACATGGTTTCCCTGGCAGAACGAAATCCAC 1804

Db 1751 GACATCCCATATGGATTCAGACAGTTGCTTCCCTTACGATCCCATCGC 1810

Qy 1805 AGGTGTTTGGCACCCTTACAGGYACCAAAAGCTATTGGCAAGCTTCAACGTA 1864

Db 1811 AACAAATTGATGATTTGCAAGAACCTCTAAAGATTATTAAACAAAGCAACGAA 1870

Qy 1865 TTTTCA 1871

Db 1871 TTATCA 1877

RESULT 12

US-11-050-829-13

; Sequence 13, Application US/11050829

; GENERAL INFORMATION:

; APPLICANT: KIRA, IKUO

; APPLICANT: YOKOZEKI, KENZO

; APPLICANT: SUZUKI, SONOKO

; APPLICANT: MIHARA, YASUHIRO

; TITLE OF INVENTION: MUTANT MICROORGANISM AND METHOD FOR PRODUCING PEPTIDE USING THE

; TITLE OF INVENTION: SAME

; FILE REFERENCE: 265063US0

;	CURRENT APPLICATION NUMBER:	US/11/050, 829	Qy	905	TACAGGAGGTAAACCCAGCTGTGATGTTGGTTCCTTGACCGGAAGATGCTT	964	
;	CURRENT FILING DATE:	2005-05-07	Db	911	TAACTAACGTGAACTGCTTAACTGAGCTTGGATGAACTTGTGCAAGATGCT	970	
;	PRIOR APPLICATION NUMBER:	US 60/617, 060	Qy	965	ATGGAACATTAAAGACCTTACCATGTTGGGATAAAGCAAAAACACTGGATT	1024	
;	PRIOR FILING DATE:	2004-10-12	Db	971	ACGGGTTTCAAACTTAAAGCTTAAAGCTTAAAGCTTAAATCAGAAGCAAAATTA	1030	
;	NUMBER OF SEQ ID NOS:	22	Qy	1025	TAGTCSGGAACCTGTGTTATGCGGGTTGGTTGGTACGGAAACTTATTTAGGTG	1084	
;	SOFTWARE:	Patent In version 3.3	Db	1031	TGGTGCACCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGGAG	1090	
;	SEQ ID NO:	13	Qy	1085	ATATCCATTGAGAAAAACCAGATTAACTTATGAGAACATTGACAACCTTT	1144	
;	LENGTH:	2024	Db	1091	ATATGAAATTGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	1150	
;	TYPE:	DNA	Qy	1145	TCAAATTACCTAAAGATGAGGAAACTTGTGCCCCCTGGAAAGCTAACATTGTGTT	1204	
;	ORGANISM:	Empedobacter brevis	Db	1151	TTAAATTACTTAAAGATAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA	1210	
;	FEATURE:	Conservative	Qy	1205	CAGGAGCAACGAAATGGAAACATTTGAAACAGTGGCACCCAAAGTAGAGCAAAA	1264	
;	NAME/KEY:	CDS	Db	1211	CGGAGTAACTGAACTGAAATGTTGATGCTGGCACCCAAAGTAGTAAACGCAAA	1270	
;	LOCATION:	(61) .. (1908)	Qy	1265	AACATATCTTCAACCTCAGGGAAACTTGGGTTGACAAGTTGAGTACAGATCT	1324	
;	US-11-050-829-13		Db	1271	AAATTTTATTCGAAAAATGCTTAAATAGCTTTAAACCAACATACAAACACTT	1330	
Query Match	Best Local Similarity	39.8%	Score	771; DB 10;	Length	2024;	
;	Matches	1144;	Pred.	No. 7.8e-201;	Indels	3;	
;	;	0;	Mismatches	600;	Gaps	1;	
Qy	125	CAGCTGGGACAGGGCTATGTTAGATGATTCATTATGAAAGGCCAGAGTAGCAATTCCA	184	Db	1278	AAATTTTATTCGAAAAATGCTTAAATAGCTTTAAACCAACATACAAACACTT	1330
Db	134	CAAAAGGGATTCTGTTATGTTGCAATTAGCAAAATTAGCAAACTTAATCCGA	193	Qy	1325	GGGATGATATGTAACGACCCATAAACTGTTGGGTTAAATTCAAATCAA	1384
Qy	185	TGGGAGATGGGAAAAAATTAACTTACGGATCTACAGCTTACAGCAAAAGACAATTCCA	244	Db	1331	TTGACGAAATATGTTGGATCTAACCTCAGTGGCTTATTCAGGAGGTTTAAAGA	1390
Db	194	TGGCGGAGTTGACAAAGTTTACAGCTTAACTTACGGCAAAAGTAAACAAACAT	253	Qy	1385	ACCGAACACGGGAGPATATGGTAGATGATGACGCTTGCCTGCTGATGTC	1444
Qy	245	ATCCAGTTTGTCTCAATAGAAACGCCCTAACCGTTTCACTTATGGCCAGAACGATA	304	Db	1391	CTCGTTCAGAAAGAAATATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1450
Db	254	ATCCCGTTTGTAAATGTAACGCCCTTACAGTGGCTTATACAGTGGCTTATGAAATCA	313	Qy	1445	TGGTTATCATACGGAACCGTTGACGGAGAACCTGACGATAGTAGGCCCATCAAAACT	1504
Qy	305	AAAAAGCTTGGAAACTTCCCCTAAAGTATCGCTTACAGCTTAACTTCCCTTACAGG	364	Db	1451	TGGTGTATCATACGGAACCTGACGATAGTAGGCCCATCAAAACT	1510
Db	314	AGAAATCGTTAGAAATTTCCTACAGAAATTCGCGAAAGGTTTATTTTACCAAG	373	Qy	1505	TTCTCAAAAGTTCTGACAGGAAAGACGGGAACTATGTTGTCAAACTGATTGAGCTT	1564
Qy	365	ATGTCGGCAAGTGGTGGATGAGTGGGAAACTTACGGCTTACGTTACCTACA	424	Db	1511	ATTAGTGGTTTCTACTACGGGAAGACGCTGATATGTTGTAATTTGTTGTT	1570
Db	374	ATCTGAGGAAATGGTGGCAAGGTTGAGCTTGGGAAATTGAGCTTGGCTTAC	433	Qy	1565	ATCCGAATGATGCGAGGAAACTTACGGGAAATATGCTGATCAATGTTGTT	1624
Qy	425	GCAAGGATAAAAGGAAATCTGATGAAAGTACGGATACCTATGATGGCTTGAATGGTTAC	484	Db	1571	ATCCCTAAAACCGCAAAATTAAACAAATTATGCTGATCAAAATTGTTGTT	1630
Db	434	CAAAAGTAAAGGCAATTGAGCAAGTGGCTTACGATGAAATGGCTTAC	493	Qy	1625	GTGGTGGAGATCATGGGGAAATACGGAAATGGTTGCAAAAGCGCCTGACTC	1684
Qy	485	AGAAAANTCTCAAACAACTATAATGGCAAAAGGGCTCTGGATTCTCAGGCT	544	Db	1631	GTGCGAAATATTGGCGGAAATATGCTGATCAAACTGCTGATCAAACTGCTG	1690
Db	494	CTAAAAAACTGAGAAATTACGAAAGGAACTTATGGTAAATTCTGAAATTCTGTT	553	Qy	1685	CAGGATGGTGGTCAAAAGGTGAATTGCAACGCTTCAAAAGAGCTTCACTGCT	1744
Qy	545	TCTATTCTACCGTCGGATGGTGTCAAACACCCGGAGCTTGAAGGGCTCTCCCACAGG	604	Db	1691	CGAAATAAAGAAACAAATGTAACGATGCTGATGTTGAGCATATTTAAAGA	1750
Db	554	TTTATTCGACAACTTCACTGCAACGTTGGTTAATTCGATCAAACTCTAAAGCGTTGCAAG	613	Qy	1745	GACATCGCATTATGGTTAGGACCTTACAGCTTACGTTACAAACTCATGGTTCCCTG	1804
Qy	605	CTCCCGTAACTGAGCTGGTATATGGGCAAGACTTCCACATAATGGCTTGAATTGTTTC	664	Db	1751	GACATCGCAATTGTTGAGATGTCAGTTGCAACAGTTCAGTCACTGCTG	1810
Db	614	CGCCCGTAACTTACCAATTGGTTTACGATCATATGGATTATCTGAAATTC	673	Qy	1805	AGGTGTTTGTGACCTTACGGTACCAAAAGCTTACGTTACGCTTCACTGCTG	1864
Qy	665	AGGATGCTTAACTTACATGCAACCCGAAACTTCACTGAACTTACGGCTTAC	724	Db	1811	AAACAAATTAAAGGAACTTCAATGTTGAGATGAACTTCACTGCTG	1870
Db	674	ATGATTCTCTCCTATTGACTTGTGTTTACGTTTACGATGTTACGATGTTAC	733	Qy	1865	TTTTCA 1871	
Qy	725	ATCAATTAAAGGCAAAATTGATCAAGAGCCATAAATATACTTTTGCAGAAG	784	Db	1871	TTTATCA 1877	
Db	734	ATAAAGCTCGAAACCTTGTGATATCTCAATAAGATAATTAGATTTATGCT	790	Qy	845	ACCTGTTAACTCCGGACTATGGTAAATTCGGTAACTTGGTACATGAAATTCT	904
Qy	785	CAGGAACAGGGGGAACTCAAGAAAAGTATTGGTAAACCTCGTACAAATTGGA	844	Db	851	ATTATTTGCGCATCCGATTAGCTGATGTTACGATCAATTGCAAGTAACTTAC	910

RESULT 13

US-11-085-576-11

; Sequence 11, Application US/110855576
; Publication No. US20050227325A1

PESHTICHT 14

us-10-763-179-17
; Application US/10763179
; Publication No. US20040204577A1

GENERAL INFORMATION:

APPLICANT: HARA, SEIICHI

APPLICANT: YOKOZU, KENZO

APPLICANT: ABE, ISAO

APPLICANT: TONOUCHI, NAOTO

APPLICANT: JOJIMA, YASUKO

TITLE OF INVENTION: NOVEL PEPTIDE-FORMING ENZYME GENES

FILE REFERENCE: 247848050

CURRENT APPLICATION NUMBER: US/10/763,179

CURRENT FILING DATE: 2004-01-26

PRIOR APPLICATION NUMBER: JP 2003-16765

PRIOR FILING DATE: 2003-01-24

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 17

TYPE: DNA
ORGANISM: Pedobacter heparinus

FEATURE: CDS

NAME/KEY: LOCATION: (61) ..(1935)

OTHER INFORMATION:

US-10-763-179-17

Query Match 35.9%; Score 694.6; DB 8; Length 1974;

Best Local Similarity 61.7%; Pred. No. 8.2e-180; Mismatches 699; Indels 15; Gaps 2; Matches 1149; Conservative 0; MisMatches 699; Indels 15;

Qy 79 TGCCTAACTTACGGCTTACAGCGTTACATGCTCAACAGCTGCCACTCG 138

Db 82 TCCCTCATTTCTCCTTATTACCGTTTCGCTCAACAGTCCGACTCT 141

Qy 139 GCTTGTAGATGAGATCATTTGAAAGA CCGAGTAGCAATTCCATGGAGATEGAA 198

Db 142 GCTTATACTGCTGAGACTATACCCAAATTAGAAAGCTGATCCCTATGGGATGGATT 201

Qy 199 AAATTATTACTGCTGATCTACAGTCCAAAGACAATTCCAGTTATCCGTTTGCTC 258

Db 202 AAGCTTATTACGGCATTACATCCCACAAAGCAAGAATTCCCTTATGCTC 261

Qy 259 AATAGAACGCCCTACAGGTTCACCTTATGGCGAACGGAATTAAAGCTTGGAA 318

Db 262 AACCGTACTCCTTATACCGTTTCGCTTATGGCAAACAAATTAAACAGCTTGGC 321

Qy 319 AACCTTCCAAAATGATGCTGTAAGGCTATTTTGTGTACCGGATGTCGGCAAG 378

Db 322 CCCTCTCGCTTATAAGAAGCTTACCTTATGGATTACGGATTAAGGGCAA 381

Qy 379 TGGATGAGGCAAGGGTGAATTGAGATATAGTACGCTGGACAGCTAGC---AAAGATAAA 435

Db 382 TGGATGAGGCAAAAGGGGGCTCATGGATTCTCATCGGGCTTACGGCAAAATAGCGAACCAA 441

Qy 436 AAAGCAATCGTGAAGTACGGTACCTTATGGCTGATGGTTACAGAAATCTC 495

Db 442 ACGGPATATGTGAAGCTGGATACCTTATGGCTGATCGTCAAGAACATT 501

Qy 496 AAAAACTTAATGGCAAAAGGGGGCTCATGGATTCTCATCGGGCTTACGGCAAAATAGCGAACCAA 555

Db 502 CCTGGAAACACCGTAAACCGTATTACCGTATCTACCGTTACGGCTTATGCTACT 561

Qy 556 GTGGATTGGTCAAAACACCCGAGCTGAGGCGTTCTGAGGCTCCAGGCTCCGTAACA 615

Db 562 GCTGCCCTACCGATSGCATCCATTAAAGCGTAAAGCTGGCTTACCGTCAAC 621

Qy 616 GACTGTTATGGCAGACTTCCACCATATGGTATGTTCTGGATGCTT 675

Db 622 GACTGTTATAGGCAATGTTCTCATCACATGGCACCTGTTGGATATCTT 681

Qy 676 ACATCATGGTAAACCTTGGTCCCTCGTCCAAACCCATTACACGGATCAATTAAAG 735

Db 682 AGCTTATATATACTTCGGGTTACCCGACTCAGCAATTACGGCCATCC 741

Qy 736 GCCAAAAATTCAAGATCAAAGGCGATAAAATAACTTGTGAGAAGCAGCG 795

Db 742 AAACCCPTGATTTGGTTCCGGTAAAGACAATACGGTTTCTCAACCTGGCCCTTA 801

Qy 796 CGGAACATCAAGAAAGTATTTGGTGAATTTGGATCAACTTGTGTTAG 855

Db 802 AAAACATCACCAAAAAATAATTATGGCATACCATAGATGATGATCATGTCG 861

Qy 856 CATCCGACATGATGATGATTTGGAAATCGGTGTATCAAGAATCTTACAGGAGTA 915

Db 862 CATACCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 921

Qy 916 AAACAGCTGTGATGGTGGTTGGTTCTTGTGAGGAGATCCATTGAAACATT 975

Db 922 AAACCTGCAAGTTGGTAGTGGGGCTTCTGGAGAGACCTTACGGTACGGCT 981

Qy 976 AAGACCTTACCATATGATGATGATGATGATGATGATGATGATGATGCGGGA 1035

Db 982 AAAACCTATCAGGCCATCGAAAAACAAATCCATCTCAAAACACCTCGTTAGGGC 1041

Qy 1036 CCTTGTATCATGGCTGGTTGGTCTGCAAGGAAACATTAGTGATATCCAAATT 1095

Db 1042 CCCTGTTACATGGCTGGCTGGCTGGCAAGAAATACGGGAGCTTCGGGATTT 1101

Qy 1096 GAGAAAAAAACCAGTATTACTTATGGAAACATTGAAACACCCATTTCGATTAC 1155

Db 1102 GGACGCCAACAGTACTCATACGGAAAAATGTGAGTCCCTTCCTTATGGAAATC 1161

Qy 1156 CTAAAGATGAGGAAACACTGGCCCTTCGGAAAGTAACTTGTGAACTTGTGAACTAC 1215

Db 1162 CTCAARGAGGCCATGGCAAAATTTGAGGAAACATTATGCTACTGGCCAAAT 1221

Qy 1216 GAATGAAACATTCCAACAGTGGCCACAAAATGAGACAAAAAAACTATAPACTC 1275

Db 1222 GAATGAAAGAAATTAGCTCTGGCACCTCAGGTTACAGAAGAGACATTAACTTC 1281

Qy 1276 CAACCTCAGGGAAACTTGGATTGACAGATTGACAGTTCTGGGATGATAT 1335

Db 1282 CAGCCCAATGCAACTGAGTTTGGAGAGTACGGGAGCCGAGGTTGGAGATGATAT 1341

Qy 1336 GTAAACAGACCTTAATAAACCTGTTGGCATCAAGTGGGTAAATTCAAACCGAACACGG 1395

Db 1342 GTAATGATCCAACTCACCTGTCCTTATCAGGTGGCATACAACCGAACCCGG 1401

Qy 1396 GAGTATATGGTAGATGATCAACGTTGCGCTGAGTGCCTGTGATGGTTATGAA 1455

Db 1402 GAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1461

Qy 1456 ACGGACCGTTGACCGAGGACCTGAGCTGAGTATGCGCTTACGGGATGATGGGTA 1515

Db 1462 ACAGGCCCTCAGTCCGACCTGATGATGATGATGATGATGATGATGATGATG 1521

Qy 1516 TCTTCAACAGAAACAGACGGGACTATGGTCAAAACTGATGATGATGATGATG 1575

Db 1582 ACACCAAATCCTGTTACCCATTACGGTAAACCTGATCATGGTGTGTTACGGATGGT 1641

Qy 1624 CGTGGTGGAGTCACTGGGGAAATACCGAAATGGTTTCGATAMAGCGCAGGGCTTGACT 1683

Db 1642 CGGGGGAGGATCACTGGTCAAAACTGATGATGATGATGATGATGATGATGATG 1701

Qy 1684 CCAGGAGTATGATGCAAAAGGTGAATTGGAAATGCTGATGATGATGATGATGATG 1743

Db 1702 CCTGGCAAAATTACAAAGTAAACTATGGCTTCCGGATSTAGCCCATACCTTAA 1761

Qy 1744 GGACATTCGCAATTATGGTTCAGGTACAAAACCTCATGTTCCGGTCAACGGAAATCCA 1803

Db	1462	ACAGAGCCCTCAGTTCGACCTTACACTTACCGGCCGATTGGCAAACCTGGTGTAA	1521
Qy	1516	TCTTCACAGAACAGACGGGACTATGTTGTCAAACTGATGACCTTATCCGAATGAT	1575
Db	1522	TCAACCACGGTAGGGATTCAGGATTAATGGTGGAAAATCTGGAAAGAT	1581
Qy	1576	GCAGCAAGTTATCAAGAAAAACA-----ATGGCTGGATATCAAATGATGGTA	1623
Db	1582	ACACCAAAATCCGTACCTAACCTTAAACCTGATACAGATGGCTGTTA	1641
Qy	1624	C GTGGTGAGATCATGGGGAAATACCGAAATGGTTTGATAAAAGCAGCCCTTGACT	1683
Db	1642	CCGGCGGAGATCATGGTGGAAATACCGTAAATAGCTTGTAAAACCGAGCCCTTTGTT	1701
Qy	1684	CCAGGTATGGTGGAAAAGGTGAAATTGAAATGCCAGACCTTGCGCATACCTTCAAAAAA	1743
Db	1702	CCTGGAAACAAATTACAAAGTAAACTATGCCCTTCGGATGTAGCCATACCTTTAAAAAA	1761
Qy	1744	GGACATCGCATTATGGTTCAAGTACAAACTCATGTTTCGGTGGAGACGAATCCA	1803
Db	1762	GCCCCACGGCATATGATCCAGGTCCGAATTATGTTCCCTGACCGGAAATCCA	1821
Qy	1804	CAGGTGTTTAGCACCTTATACAGCTTACAAAGCTTCCGAAAGCTACCCAAACGT	1863
Db	1822	CAGGAGTTATGGACATTACAGGCCGAACTGGGATTTCAGAAAAGCTACGATAGG	1881
Qy	1864	ATTTTCACGATGTGAAACATGCCACATACATCGAAATTCTGTCTCAAGATTAGCAG	1923
Db	1882	ATCTTCAACGATGTAACAAATGCAATTACGGAAACGTAACTGAAACCTTAAAC	1941
Qy	1924	GTA 1926	
Db	1942	GGA 1944	